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GenCore version 5.1.6
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using sw model protein search, OM protein August 10, 2004, 16:12:27; Search time 12.0425 Seconds (without alignments) 1509.673 Million cell updates/sec Run on:

US-09-811-367B-1

1023 1 MIDSVIYSMLELPTATQAQN......GLQASSCEVPLHGVCKKVRL 189 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	$\overline{}$				natural killer cel	killer		natural killer cel	HIV gp120-binding	NK-cell receptor P	lectin, galactose/	lymphocyte early a	type II lectin-lik	asialoglycoprotein	C type lectin, B l	asialoglycoprotein	lectin M-ASGP-BP p		surface	protein	hepatic lectin - r	lectin	lectin	natural killer cel	phospholipase-A(2)	hepatic lectin hom	Ly-49D-GE antigen	-	NKR-P1 protein hom
SUMMARIES	ID	159421	I38700	I50146	A46467	PT0372	PT0374	PT0375	154524	A46274	A35917	JX0209	JH0822	JC7608	S13165	T28141	S29855	A42230	A30573	A45813	B46467	LNRTL	LNRT2	LINHUI	I49361	S48719	WMVZF2	I49049	T28140	C46467
	DB					N																			~	7	⊣	~1	ď	7
	Length	188	225	257	227	233	231	216	240	404	223	304	199	237	301	156	284	306	262	262	223	284	301	291	262	1487	9	260	170	C)
s s	Query Match		•	18.9	ω,	18.6	17.8	17.6	17.4	17	Н	17	7.	16.5	9	16.2	9	16.1	15.8	S	15.7	15.7	15.7	15.4	15.3	15.2	15.0	14.8	14.6	14.5
	Score	ı N	201	193	191	190	182	180	178.5	176	175.5	174.5	174	169	167	166	165	164.5	162	162	160.5	160.5	160.5	157.5	157	156	153.5	151.5	149	148.5
	Result No.	, r-1	2	٣	4	ហ	9	7	80	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Kupffer cell recep	secretory phosphol	secretory phosphol	asialoglycoprotein	mannose receptor,	aggretin alpha cha	agkisacutacin beta	phospholipase A2 r	Ly-49G.2 antigen -	Ly-49G.1 antigen -	chondroitin sulfat	phospholipase A2 r	pancreatitis-assoc	pancreatic stone p	natural killer cel	scavenger receptor
A28166	B56395	A56395	LNHU2A	T42710	PC7027	JC7135	A49707	I49053	I49052	A47171	A53210	S29822	A28351	I49363	JC7595
2	7	7	H	7	N	Ŋ		~	7	N	0	7	7	7	N
550	1326	1465	311	1479	144	146	1458	267	280	3562	1463	175	165	366	742
14.5	14.3	14.3	14.3	14.2	14.0	13.9	13.8	13.7	13.7	13.6	13.5	13.4	13.4	13.4	13.4
		'n	#6	ıs.	5.	142	141.5	0.5	2.5	9.5	3.5	7.5	137	37	13.7
148.5	146.5	146.	Ä	145	143		14	14	14	13	13	13		-	

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		000000000000000000000000000000000000000
:	21	-

mast cell function associated antigen - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: IS9421

Riguthmann, M.D.; Tal, M.; Pecht, I.
Riguthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is another C A;Reference number: 159421; MUID:96016176; PMID:7568140
A;Accession: 159421 MUID:96016176; PMID:7568140
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-188 <RES>

A; Cross-references: EMBL: X79812; NID: g1020141; PIDN: CAA56208.1; PID: g1020142 C;Genetics: A;Gene: mafa

Gaps 1; Length 188; 51.4%; Score 525.5; DB 2; Length ilarity 53.5%; Pred. No. 4.8e-42; Conservative 29; Mismatches 57; Indels Query Match Best Local Similarity Matches 100; Conserv 9 9 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL Dp à

61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120 à

61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120 g

121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFYQTCGAINKNGLQASSCEVPL 180 g ð

181 HGVCKKV 187 :|:|| QWICEKV 186 à

Db

hNKR-Pla protein - human

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: Oz-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Date: Oz-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I18700
R;Lanier, L.L.; Chang, C.; Phillips, J.H.
A;Taile: Human NKR-PLA: Maisulfide-linked homodimer of the C-type lectin superfamily e A;Reference number: I18700
A;Atclession: I38700
A;Accession: I38700
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

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J. Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated ki
A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: A46467
                                                                                                                A; Molecule type: mRNA
A; Residues: 'MHILCT',1-27 <GIO>
A; Residues: 'MHILCT',1-27 <GIO>
A; Cross-references: GB:M77676; NID: 9200058
A; Cross-references: GB:M77676; NID: 9200058
A; Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence
K; Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.
J. Immunol: 149, 1957-1963, 1992
A; Title: Genomic structure and strain-specific expression of the natural killer cell re
A; Reference number: A46502, MUID:92388663; PMID:1517565
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                      N.Alternate names: NKG2-A, NKG2-B

N.Contains: natural Killer cell receptor group 2, splice form B

C.Species: Homo sapiens (man)

C.Species: Homo sapiens

C.Species: Homo 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 IGLR---NNSGWRWEDGSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 POOKSSSSKPSCSCLVAITLGLL-TAVLLSVLLYQ-----WILCOGS-NYST-CASCPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAF -- CW
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iller cell
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A;Molecule type: mRNA
A;Residues: 1-95,114-233 <HOUZ>
A;Residues: 1-95,114-233 <HOUZ>
A;Cross-references: GB:X54868; NID:g35058; PIDN:CAA38650.1; PID:g35059
A;Experimental source: natural killer cell
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.7%; Score 191; DB 2; 27.4%; Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: PT0372
A,Molecule type: mRNA
A,Residues: 1-233 4HOU1>
A,Experimental source: natural killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: KLRC1; NKG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
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                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 VEEKDWINSSLEFCLARDSHLLVITDNQEMSLLQVFLSE--AFCWIGLR----NNSGWRWED 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|| | ::| ||:| | :: | HTVNPWNNSLADCSTKESSLLIEDENTRDELIEPTIGENFSLSEKNWKWIN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ASCPS----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPRPPFSHVCPNAWVGFQGKCYYFSDTESDWNSSREHCHRLGASLATLDTKEEMEFMLQY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORPADRWIGIHRAEGDEHWTWADGSAFTNRPVFELRGGGRCAYLNGDGISSALCHSEKFW 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matural killer cell receptor Pl - mouse
N;Alternate names: NKR-Pl protein
C;Species: Mus musculus (house mouse)
C;bate: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
C;Accession: A46467; A46502; Ā46456
R;Giorda, R.; Trucco, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 VVTGLSVSVT----SLIQKSSIEKCSVDIQQSRNKTTERPGLLNCPIYWQQLREKCLLFS
                                                                                                                                                                                                                                                                              SCSCLVAITLG
                             PIDN: AAA21605.1; PID: 9544496
                                                                                                                                                                                                                                                                                                                     1 MDQQAIYABINLPT-----DSGPESSSPSSLPRDVCQGSPWHQFALKLSCAGIILLVL-
                                                                                                                                                                                                                                                                                                                                                                                               -SCPSCPDRWMKYGNHCYYFS
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-257 cBRS.
A:Residues: 1-257 cBRS.
A:Cross-references: GB:M88072; NID:g505324; PIDN:AAA48558.1; PID:g505325
C;Superfamily: C-type lectin homology
F;129-241/Domain: C-type lectin homology <LCH>
            A;Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PID:954.
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>
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                                                                                                                                                 Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenetics 39, 221-229, 1994
Affitle: Linkage of a new member of the lectin supergene
A;Reference number: I50146; MUID:94164691; PMID:8119728
A;Accession: I50146
                                                                                                                                                 ; DB 2;
1.7e-11;
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Pred. No. 1.1e-10;
                                                                                                                                       Query Match
19.6%; Score 201; DB
Best Local Similarity 26.0%; Pred. No. 1.7e
Matches 58; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: 150146
R,Bernot, A.; Zoorob, R.; Auffray, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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1 Similarity 26.6%;
49; Conservative 2
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Best Local Similarity
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16;

Indels

74

5

Length 216;

--RNNSGWRWED 145

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Nylternate names: integral membrane protein NKG2-D

Nylternate names: integral membrane protein NKG2-D

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 05-May-2000

C;Accession: PT0375; S15671; S1910

R;Houchins, J.P.; Xabe, T.; NScherry, C.; Bach, F.H.

A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I:

A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I:

A;Reference number: PT0372; MUID:91178434; PMID:2007850

A;Reference number: BT0372; MUID:91178434; PMID:2007850

A;Residues: 1-216 <HOU>
A;Residues: 1-216 <HOU>
A;Cross-references: EMBL:X54870; NID:g35562; PIDN:CAA38652.1; PID:g35063

A;Reperimental source: natural killer cell

A;Note: translation of nucleotide sequence is not complete
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R; Adamkiewicz, T.V.; McSherry, C.; Bach, F.H.; Houchins, J.P.
Immunogenetics 39, 218, 1994
A; Title: Natural killer lectin-like receptors have divergent carboxy-termini, distinct A; Reference number: 154524; MUID:94102823; PMID:8276468
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C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 CLVAITLG------LLTAVLLSVLLYQWILCQGSNYSTCASCPDRWMKYGNHCYY
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C;Superfamily: natural killer cell receptor P1; C-type lectin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.6%; Score 180; DB 2; 26.8%; Pred. No. 1.6e-09; iive 31; Mismatches 52
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Pred. No. 2.4e-09;
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28.6%;
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A;Gene: GDB:KLRC2; NKG2-C
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les 42; Conserv
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A; Residues: 1-240 <RES>
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MyAlternate names: NKG-C
G)Species: Homo sapiens (man)
C)Species: Homo sapiens (man)
C)Bate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
C)Accession: PT0374
R)Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
B,FHouchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
B,FAccession: PT0374
B,FACCEST
B,FACCE
                                   A,Map position: 12pter-12qter
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: alternative splicing; glycoprotein; transmembrane #status predicted F;71-98/Domain: transmembrane #status predicted F;71-98/Domain: C-type lectin homology <br/>Kill9-229/Domain: C-type lectin homology <br/>Kill9-130,181,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-130,147-229,208-221/Disulfide bonds: #status predicted
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C,Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane protein
F;71-96/Domain: transmembrane #status predicted <TRA>
F;71-96/Domain: transmembrane status predicted <TRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 233;
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; Pred. No. 1.9e-10;
35; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%; Score 190; 27.8%; Pred. No. 1
A; Cross-references: GDB:138773; OMIM:161555
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Matches 47; Conservative
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9

Gaps

15;

Indels

70; DB 2;

RESULT

Length 240;

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A;Title: Molecular cloning, expression, and chromosomal localization of the human earli mitting receptors.
A;Reference number: JH0822; MUID:93340630; PMID:8340758
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Ross-references: 1-199 <LOP>
A;Cross-references: GB:Z22576; NID:g397938; PIDN:CAA80298.1; PID:g397939
A;Note: the authors translated the codon CAA for residue 110 as GLu
A;Note: the authors translated the codon CAA for residue 110 as GLu
J. Immunol. 150, 4920-4927, 1993
A;Title: Expression cloning of the early activation antigen CD69, a type II integral me
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A.Residues: 1-199 **RES-
A.Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1; PID:g291898
R.Santis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid,
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212
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                   A46274

HIV gp120-binding C-type lectin - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21.Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
C;Accession: A46274
R;Curtis, B.M.; Scharnowske, S.; Watson, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89; 8356-8360, 1992
A;Title: Sequence and expression of a membrane-associated C-type lectin that exhibits CI
A;Reference number: A46274; MUID: 92390446; PMID:1518869
A;Accession: A46274
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-404 cCUR>
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)
C;Superfamily: C-type lectin homology
F;256-377/Domain: C-type lectin homology <LCH>
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A;Title: NRR-Pl, a signal transduction molecule on natural killer cells.
A;Reference number: A55917; MUID:90378305; PMID:2399464
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C;Date: Patr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999
C;Accession: A35917
R;Giorda, R.; Rudert w h v v---
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A; Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723
C; Superfamily: natural killer cell receptor Pl; C-type lectin homology
C; Keywords: transmembrane protein
F; 94-210/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 176; DB 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 PQQKSSSSKPSCSCLVAITLGLL-TAVLLSVLLYQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.2%; Scc. No. ,c
30.7%; Pred. No. ,c
'... 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHGVCKK 186
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A35917
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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R.; Esch, F.; Sanchez-M

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lectin, galactose/N-acetylgalactosamine-specific - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: JX0209; PX0009
R;Sato, M.; Kawakami, K.; Osawa, T.; Toyoshima, S.
J. Biochem. 111, 331-336, 1992
A;Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalactos
                                                                                                                                                                                                                                                                                                                        A;Accession: JX0209
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: 1-304 cSAT>
A;Cross-references: GB:S36676; NID:g249360; PIDN:AAB22171.1; PID:g249361
R;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
B;Cochem. 104, 600-605, 1988
A;Title: Purification and characterization of a lectin-like molecule specific for galac A;Reference number: PX0009; MUID:89197865; PMID:3241002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 EQNFLQNRLANVVSWIGLTDQNGPWRWVDGTDFEKGFKNWAPLQPDNWFGHGLGGGEDCA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: PX0009
A,Moleule type: protein
A,Residues: 102-120;137, X', 139-151 < 0DA>
A,Residues: 102-120;137, X', 139-151 < 0DA>
C,Superfamily: hepatic lectin; C-type lectin homology
C,Keywords: glycoprotein; lectin; macrophage; transmembrane protein
F;36-61,Domain: transmembrane #status predicted <TRA>
F;36-61,Domain: C-type lectin homology < CLR>
F;173-296,Domain: C-type lectin homology < CLR>
F;74,166,Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 EMSLLQVFLSEAFCWIGLRNNSG-WRWEDGSPL----NFSRISSNSFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.1%; Score 174.5; DB 2 27.5%; Pred. No. 7.2e-09; Live 27; Mismatches 61
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143

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Ciype lectin, B locus - chicken
(Species: Gallus gallus (chicken)
Cybate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
CyAccession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
Berinte, S.; Kaufman, J.; Beck, S.
R;Milne, S.; Kaufman, J.; Beck, S.
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor gene
                                                                          KETFSNFSSSTIMEFGALDTLGGSTNAILTSWLAQLEEKQQQLKADHSTLLFFHLKHFPMD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: T28141
A;Accession: T28141
A;Actives: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DAB
A;Residues: 1-156 AMIL>
A;Residues: 1-156 AMIL>
A;Residues: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A;Rxperimental source: clone cB12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N'Alternate names: hepetic lectin
C'Species: Mus musculus (house mouse)
C'Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C'Accession: Sl1165
R'Sanford, J.P.; Doyle, D.
Biochim. Biophys. Acta 1087, 259-261, 1990
A;Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of re
A;Reference number: Sl3165; MUID:91027942; PMID:2223888
                                                                                                                                                                                                 --VQTCGAIN-----KNGLQASSCEVPLHGVCKKVR
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A, Cross-references: EMBL:X53042; NID:g53104; PIDN:CAA37211.1; PID:g53105

C, Superfamily: hepatic lectin; C-type lectin homology

C, Keywords: glycoprotein; liver; transmembrane protein

F;170-293/Domain: C-type lectin homology <LCH>
                     88 YFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS-LLQVFLSEAFCWIGLRNNSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :99
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25.9%; Pred. No. 3.6e-08;
cive 29; Mismatches 72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TCGAINKNG-LQASSCEVPLHGVCKKVR 188
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                                                                                                                                                                                            144 EDGSPLNFSRISSNSF
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A; Introns: 17/1; 74/3; 110/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Les 55; Conserv
                                                                                                                                                                                                                                                                       179 VDQTPYN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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                                                             A; Illue: Structure of the gene couling for the numban early lymphocyce activation antigen captors.

A; Reference number: $60753; MUID:94298875; PMID:8026529

A; Reference number: $60753; MUID:94298875; PMID:8026529

A; Reture: preliminary

A; Molecule type: DNA

A; Readaus: preliminary

A; Molecule type: DNA

A; Residues: 1-199 < SAN>

A; Residues: 1-199 < SAN>

A; Residues: 1-199 < SAN>

A; Comment: This protein is the earliest inducible cell surface glycoprotein expressed in C; Generics:

C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: C; Generics: Generics: C; Generics:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type II lectin-like immunoreceptor - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: JG7668

R;Huang, X.; Yuan, Z.; Chen, G.; Zhang, M.; Zhang, W.; Yu, Y.; Cao, X.

B;Jechem: Biophys. Res. Commun. 281, 131-140, 2001

A;Reference number: JG7608; MUID:21092797; PMID:11178971

A;Reference number: JG7608

A;Molecule type: mRNA

A;Residues: 1-237 <HUA.

A;Residues: 1-237 <HUA.

A;Residues: 1-237 <HUA.

A;Residues: 1-237 <HUA.
Bur. J. Immunol. 24, 1692-1697, 1994
A,Title: Structure of the gene coding for the human early lymphocyte activation antigen
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C;Comment: This receptor, highly homologous to the group of macrophage/hepatic lectins
cell, especially in migrating, antigen capturing and processing.
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:45-69/Domain: transmembrane #status predicted <TMM>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 10, 2004, 16:05:41; Search time 7.35929 Seconds (without alignments) 1337.256 Million cell updates/sec Run on:

US-09-811-367B-1 Title:

Perfect score:

1 MIDSVIYSMLELPTATQAQN.........GLQASSCEVPLHGVCKKVRL 189 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	NKGA PANTR	CD94 MACMU	CD94 HUMAN	CD69_MOUSE	CD94_PANTR	NK11 MOUSE	NKGA HUMAN		NKGC HUMAN	NKGD MACMU		NKGD HUMAN	NKGE_HUMAN	NKGE PANTR	NK13 RAT	CLE2_HUMAN	MMGL_MOUSE	CD69_HUMAN	LECI_MOUSE	MMGL_RAT	LECH_MOUSE	NKGC_MACMU	LY4A_MOUSE		LECH_RAT	LECH HUMAN	V239 FOWPV	LECI_RAT	V008 FOWPV	KLR4 MOUSE	NK14 MOUSE	KUCR RAT	PBCG_MESAU
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EMBL; AF259055; AAF86965.1; -. EMBL; AF259056; AAF86966.1; -. EMBL; AF350005; AAK83792.1; -.

009049 mus musculu P70194 mus musculu	P81509 crotalus ho	P49260 oryctolagus O60654 mis misculu	090953 gallus gall	P49259 bos taurus P35230 mus musculu	P10758 rattus norv	P06734 homo sapien	P20693 mus musculu
PAP3_MOUSE	CHBB_CROHO	PA2R_RABIT KLR7_MOUSE	PGCV_CHICK	PAPI_MOUSE	LITH_RAT	FCE2_HUMAN	FCE2_MOUSE
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174	117 311	1458	3562	175	165	321	331
14.4 14.3	14.3	13.8	13.6	13.4	13.4	13.3	13.3
147	146 146	141.5	139.5	137.5	137	136.5	136.5
3.4 3.5	36 37	38 39	40	4.4	43	44	45

ALIGNMENTS

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                                                                 NKGA_PANTR STANDARD, Q95MTA; Q95MTA; Q95MTA; Q95MTA; Q95MTA; Q97MTA; Q95MTA; Q95MTA; Q95MTA; Q95MTA; Q95MTA; Q95MTA; Q95MTA; Q97MTA; Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21623889; PubMed=11751968; Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P., Guethlein L.A., Uhrberg M., Parham P., Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1. FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-B molecules by NK cells and some cytotoxic T-cells.
-1. SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
-1. SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS LEU-79 AND
                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20350666; PubMed=10894168;
Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
Parham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            þλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rapid evolution of NK cell receptor systems demonstrated comparison of chimpanzees and humans."; Immunity 12:687-698 (2000).
                                                                                                                                                                                                                                                                                                                                                Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOId=095M15-2; Sequence=VSP 003066;
-!- TISSUE SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=095MI5-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9598;
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RESULT 1
NKGA PANTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : : | | : : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21158386; PubMed=11261935;
Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 ITYAELNLQKASQDFQENDKTYHCKDLPSAP--BKLIVGILGIICLILMASVVIIVVIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 ILCQGSNYST-----CASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHIL
                                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE=20322467; PubMed=10866118;
MEDLINE=20322467; PubMed=10866118;
"L., Levy D.B., Letvin N.L.; N.L.; ANG2 family members and "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                        SMART; SM00034; CLECT; 1.
SMOSTHE, PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.5%; Score 199; DB 1; Length 233; 28.4%; Pred. No. 6.7e-12;
                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTINED (GLCNAC. . ) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (in isoform NKG2-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE94BEA3A0209984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Matural Killer cells antigen CD94 (NK cell receptor) lectin-like receptor subfamily D, member 1).
                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> L (in NKG2-A*03).
                                                                                                                                                      Glycoprotein; Alternative splicing; Polyworphism DOMAIN 71 93 SIGNAL-ANCHOR (TYPE-TRANSMEM 71 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP_003066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 6.7e
34; Mismatches
                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 NGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 NGLKSAQCGSSIIYHCK 230
        InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 28.4%;
56; Conservative 3
                         Pfam; PF00059; lectin c; 1. SMART; SMO034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                           94
1118
1119
1208
102
103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD94 MACMU
                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                             DOMAIN
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CD94_MACMU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MAVFKTTIWRLISGTLGIICLSLMATLGILLKNS -> MAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLSLMA-TLGILLKNSFTKLSVEPAYTPGPNIELQKDSDCCSCHEKWVGYRCNCYFISSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                         FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.4%; Score 198.5; DB 1; Length 179; 33.3%; Pred. No. 5.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 --SOYLFPSFETFKPKNCIAYNSKGNALDESCETKNRYICKO 176
                                                                                                                                                                                                                                                                                      Name=1; Synonyms=CD94 alt; Isold=QymXK9-3; Squence=VSP 003054; Isold=QymXK9-3; Squence=VSP 003054; ISSUB SPECIFICITY: Natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06212B4494527F07 CRC64;
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L -> LQ (in isoform 2)
                                                                                                                            SUBCELLULAR LOCATION: Type II membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                          Event Alternative splicing; Named isoforms=3; Name=1; Synonyms=CD94-A; Isofa-G9MZK9-1; Sequence=Displayed; Name=2; Synonyms=CD94-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 69
splicing of 5' exons in rhesus monkey decidua.";
Immunogenetics 53:69-73(2001).
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                                                                                                                                                                                                                                                                      IsoId=Q9MZK9-2; Sequence=VSP_003055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF190931; AAF74527.1; -. EMBL, AF190932; AAF74528.1; -. EMBL, AF190933; AAF74529.1; -. EMBL, AF294886; AAG34498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_c; l. SMART; SMO0034; CLECT; l.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Conservative
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179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P22897; 1EGG
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                                                                                                                members
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DISULFID
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Matches 5
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WESTURE-2238827; PubMed=12477932;

WEDLINE=2238827; PubMed=12477932;

Ratabner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altashul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Datchenhor D., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Saka S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Sosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Pichards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tadokoro K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                 Q13241; 043321, 043773; Q9UBE3; Q9UBC0; 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Natural killer cells antigen CD94 (NK cell receptor) (Killer cell cetin-like receptor subfamily D, member 1) (KP43).
                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98139529; PubMed=9472066;
Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
Lehrach H., Francis F., Lopez-Botet M.;
"Structure of the human CD94 C-Type lectin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=98267245; PubMed=9601951;
Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T.,
Tohma S., Inoue T., Yamamoto K., Juji T.;
"A alternatively spliced form of the human CD94 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biassoni R.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                      179 AA
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96011848; PubMed=7589107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
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                                           STANDARD;
                                                                                                                                                                                                                                                                                KLRD1 OR CD94.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Blood;
                                           CD94 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biassonı
CCD94 HUMAN

ID CD94 H

AC CLD CD94 H

DT 01-NOV

DT 01-NOV

DT 01-NOV

DT 01-NOV

DE NATURAL

OS BUKARY

OC BUKARY

OC MAMMAI

OX M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lanier
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Event=Alternative splicing; Named isoforms=3;

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                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 602894; -.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:000466; P:antimicrobial humoral response (sensu Inver. .; TAS.
InterPro; IPR001304; Lectin.C.
InterPro; IPR001304; Lectin.C.
SMART; SM00034; CLECTI.C.
PROSITE; PS00041; C_TYPE LECTIN.1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN.2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 CLSIMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
             IsoId=Qi324i-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Qi3241-2; Sequence=VSP_003053;
Name=3; Synonyms=CD94 alt;
IsoId=Qi3241-3; Sequence=VSP_00362;
TISSUB_SPECIFICITY: Natural killer cells.
SIMILARITY: Contains I C-type lectin family domain.
DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 --SQYLFPSFETFNTKNĆIAYNPNGNALDESCEDKNRYICKO 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1884D99E8D9583A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L -> LQ (in isoform 2).
/FIId=VSP_003053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.2%; Score 196.5; DB 1
Best Local Similarity 32.7%; Pred. No. 8.6e-12;
Matches 53; Conservative 25; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      003052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP
                                                                                                                                                                                                                                                                                                        EMBL, U30610, AAC50291.1; -.
EMBL, Y14287; CAA74663.1; -.
EMBL, Y14288; CAA74663.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ000673; CAA04230.1; --
EMBL; AJ000001; CAA03845.1; --
EMBL; AB000597; BAA24450.1; --
EMBL; AB010084; BAA24451.1; --
EMBL; BC028009; AAH28099.1; --
PDB; 1B6E; 15-JUN-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 AA; 20497 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC: 6378; KLRD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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176
72
174
166
132
34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing;
DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
98
61
89
152
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE II membrane glycoprotein related to a family of natural killer type II membrane glycoprotein related to a family of natural killer cell activation antigens.";

Eur. J. Immunol. 23:1648(1993)

Eur. J. Immunol. 23:1648(1993)

Signal transmitting receptor in lymphocytes, natural killer (NK) cells, and platelets

C. -- FUNCTION: Involved in Lymphocytes, natural killer (NK)

C. -- SUBENIT: Homodimer; disulfide-linked.

-- SUBCELLULAR LOCATION: Type II membrane protein.

-- SUBCELLULAR LOCATION: Type II membrane protein.

-- TISSUE SPECIFCITY: EXPRESSED ON THE SURPACE OF ACTIVATED T CELLS,

-- FUNCTION: BY the activation.

-- INDUCTION: BY the activation.

-- INDUCTION: BY the activation.

-- INDUCTION: BY the activation of T lymphocytes.

-- TYPE CONSTITUTIVE SER/THE PHOSPHORYLATION IN BOTH MATURE

-- PTM. CONSTITUTIVE SER/THE PLOSPHORYLATION IN BOTH MATURE

-- SIMILARITY: Contains 1 C-type lectin family domain.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

BENDLINE-29314711; PubMed=8100776;
Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.
                                                                                                                                                                                                                                                               Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam. PF00059; lectin c.; PFam. PRINTS, PR00356; ANTIEREZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39F8E4941D36D4F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC
                                                                                                             or-curly94 (Rel. 30, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Early activation antigen CD69.
                                               199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-TYPE LECTIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:88343; Cd69.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L23638; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22517 MW;
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                     (Rel. 30, Created) (Rel. 30, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.2%;
                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
195
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                                                                                                                                                                                                                                           Mus musculus (Mouse)
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150
166
180
199 AA;
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96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alderson M.R.;
                                                                                                     01-OCT-1994
                                                  CD69 MOUSE
P37217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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RESULT 4
CD69_MOUSE
                                                                           SOUR THE TENT TO BE A PROPERTY OF THE PROPERTY
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Score 196.5; DB 1; Length 199;

Pred. No. 9.7e-12;

Best Local Similarity

Query Match

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7,
                                                                                                                     119
                                                                                                                                           SILQVFLSEAFCWIGLRN--NSGWRWEDGSPLN--FSRISSNSFVQTCGAINKNGLQASS 175
                                                                                                                                                                                                                       73
                                                                           69
                                     17 QAQNDYGPQ----QKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYSTCASCP
                                                                           18 RGÓKDHGTSIHFEKHHEG----SIQVSIPWAVLIVVLITSLIIALIALNVGKY----NCP
                                                                                                                  74 -----SCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEM
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21623889; PubMed=11751968;
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
"Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-i- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Matural Killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1).
KIRDI OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20350666; PubMed=10894168;
Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parham P.; "Rapid evolution of NK cell receptor systems demonstrated by
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=2; Synonyms=CD94-B; IsoId=09M41-2; Squence=VSP 00356; IsoId=09M41-2; Sequence=VSP 00356; IsoSUB SPECIFICITY: Natural Killer cells: -i- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            members.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERIAL PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
    Comment=Additional isoforms seem to exist;
  79;
                                                                                                                                                                                                                                                                                                                                                                                                                       179 AA
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=1; Synonyms=CD94-A;
IsoId=Q9MZ41-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comparison of chimpanzees and humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol. 168:240-252(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [mmunity 12:687-698(2000).
      52; Conservative
                                                                                                                                                                                                                                                                                   CEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                         186 CEANFHWVCSK 196
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKG2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                         CD94 PANTR
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                                                                                                                                                                                                                                                                                   176
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      Matches
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49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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HUMAN
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Matches
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NKGA_HU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                           PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
Alternative splicing.
CYTOPLASMIC (POTENTIAL).
TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                                                                                                                                                                             SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91349596; PubMed=1880421;
Giorda R., Trucco M.;
"Mouse NKR-P1. A family of genes selectively coexpressed in adherent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
L -> LQ (in isoform 2).
/FIId=VSP_003056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Natural killer cell surface protein Pl-2 (NKR-Pl 2) (NKR-Pl.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "CDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of a natural killer cell gene complex on mouse chromosome 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: May function as signal-transmitting receptor.
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLUIAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Natural killer cells.
                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SQYLFPSFETFNPKNCIAYNPNGNALDESCEDKNRYICKQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                7244D99E8D9587E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.0%; Score 194.5; DB 1
32.7%; Pred. No. 1.3e-11;
tive 25; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymphokine-activated killer cells.";
J. Immunol. 147:1701-1708(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92013158; PubMed=1680927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 147:3229-3236(1991).
                    HSSP, P22897, 1EGG.
InterPror, IPRO01304, Lectin C.
Pfam; PF00059; lectin c, 1.
SMART; SM00034; CLECT; 1.
EMBL; AF259054; AAF86964.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    20493 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 32.7%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLRBIA OR LY55A OR LY55.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                          176
72
174
166
83
132
                                                                                                                                                                                                                                                                                                                                                                                                                179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10090;
                                                                                                                                                                                                                                       32
98
61
89
152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NK11 MOUSE
P27811;
                                                                                                                                                                                                                                                      DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NK11 | MOUSE | NK11 | MC11 | MC10 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAF--CW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQQKSSSSKPSCSCLVAITLGLL-TAVLLSVLLYQ-----WILCQGS-NYST-CASCPS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGLR---NNSGWRWEDGSPINFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUT-2003 (Rel. 42, Last amontation update)
NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating
NK receptor) (NK cell receptor A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
MEDLINE=91178434; PubMed=2007850;
Houchins J.P., Yabe T., McSherry C., Bach F.H.;
"DNA sequence analysis of NKG2, a family of related cDNA clones
                                                                                                                                                                                                                                                                                                                                                            SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
TRANSMEM 43 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.7%; Score 191; DB 1; Length 227; 27.4%; Pred. No. 3.8e-11; Indels ::ive 43; Mismatches 71; Indels ::
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S -> L (IN REF. 2).
0599A2587DF0B615 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA
                                                                                                                                                                                                                                                           HSSP, P22897, IEGG.
MGD: MGI:107540; KIrbla.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin C.
Pfam; PF00059; lectin C; 1.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 S
25689 MW;
                                                                                                                                                                                                    EMBL; M77753; AAA39366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 27.4%
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227
212
105
210
202
202
83
169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
93
122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLRC1 OR NKG2A.
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                                                                                                                                                                                                                                                                                                       Plougastel B., Jones T., Trowsdale J.; "Genomic structure, chromosome location, and alternative splicing of
encoding type II integral membrane proteins on human natural killer
                                                                                                                                                                                                                                  Kothapalli R., Kusmartseva I., Loughran T.P. Jr., Indentification and characterization of the NKG2A gene from large granular lymphocytic leukemia (LGL) cells.", Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Plougastel B., Trowsdale J.; "Sequence analysis of a 62-kb region overlapping the human KLRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOId=P26715-2; Sequence=VSP 003062;
-!- TISSUE SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                  (ISOFORMS NKG2-A AND NKG2-B).
                                               SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B)
MEDLINE=96337918; PubMed=8753859;
                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B) MEDLINE=98260668; PubMed=9598306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P26715-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X54868; CAA38650.1; -.
U54786; AAB17133.1; -.
U54783; AAB17133.1; JOINED.
U54784; AAB17133.1; JOINED.
                        Exp. Med. 173:1017-1020(1991)
                                                                                                 the human NKG2A gene.";
Immunogenetics 44:286-291(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X54867; CAA38649.1; -..
EMBL; X54868; CAA38650.1; -..
EMBL; U54786; AABL7133.1; -..
EMBL; U54783; AABL7133.1; JOI
EMBL; U54784; AABL7133.1; JOI
                                                                                                                                                                                                 Genomics 49:193-199(1998).
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=NKG2-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=NKG2-A;
                                                                                                                                                                                        cluster of
                                                                                                                                                                                                                           SEQUENCE
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111 LVITDNQEMSLLQVFLSEAFCWIGL-RNNSGWRWEDGSPLNFSR--ISSNSFVQTCGAIN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                 GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:00064888; F:transmembrane receptor activity; TAS.

GO; GO:00064889; P:annimicrobial humoral response (sensu Inver. . .; TAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.

InterPro; IPRO01349; Lectin_C.

Pfam; PF00059; lectin_C; 1.

SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VIYSMLELPTATQAQNDYGPQQKSSSSK--PSC-SCLVAITLGLLTAVLL----SVLLYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 STLIQRHNNSSLNTRTQKARHCGHCPEEWITYSNSCYYIGKERRTWEESLLACTSKNSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 WILCQGSNYST-----CASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANTS ASP-60 AND 232-TYR-ARG-233 DEL.
MEDLINE=20350666; PubMed=10894168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSGNES, QSNZ38, QSNZ40;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
NKG2-C type II integral membrane protein (NKG2-C activating NK receptor) (NK cell receptor C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.6%; Score 190; DB 1; Length 233; 27.8%; Pred. No. 4.9e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform NKG2-B) /FIId=VSP 003062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1654BD7958C81A84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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EMBL; U54785; AAB17133.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 KNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 VNRLKSAQCGSSIIYHCK 230
                   EMBL; AF023840; AAC17488.1; --
EMBL; AF464812; AAL6534.1; --
EMBL; BC012550; AAH12550.1; --
EMBL; BC053840; AAH53840.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 27.8
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                        Genew; HGNC:6374; KLRC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              70
93
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231
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                                                                                                                  PIR; PT0372; PT0372
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1118
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1103
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1180
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KLRC2 OR NKG2C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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NKGC_PANTR
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL-RNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYST----CASCPSCPDRW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                       comparison of chimpanzees and humans.";

!munity 12:687-698 (2000)

!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.

- SUBCELLULAR LOCATION: Type II membrane protein. with CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 EXTRACELLUIAR (POTENTIAL).
229 C-TYPE LECTIN (LONG FORM).
128 BY SIMILARITY.
217 BY SIMILARITY.
219 BY SIMILARITY.
100 N-LINKED (GLCNAC. .) (POTENTIAL).
178 N-LINKED (GLCNAC. .) (POTENTIAL).
60 N -> D (in allele NKG2-C*101).
233 Missing (in allele NKG2-C*101).
234 Zel69 MW, 18C04D1891B1B7CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0041; C_TYPE_LECTIN 2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKGC_HUMAN STANDARD, PRT; 231 AA.
P26717, 043802; Q9NR42;
01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-C type II integral membrane protein (NKG2-C activating NK KIRC2 OR NKG2-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGWRWEDGSPLNFSR--ISSNSFVQTCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 SHHPWVTINGLAFKHEIIDSDHAELNCAVLQVKGLKSAQCGSSIIYHCK 228
                                                                               "Rapid evolution of NK cell receptor systems demonstrated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77; Indels
                                                                                                                                                                                                                                                                                -!- TISSUE SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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28.4%; Pred. No. 9.4e-11;
live 30; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF259057; AAF86967.1; -. EMBL; AF259059; AAF86969.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P05451; ILIT.
InterPro; IRR001304; Lectin_C.
Pfam; PF00059; Dectin_c; 1.
SWART; SM00034; CLECT; 1.
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233 AA;
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                                                        Parham P.;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98350122; PubMed=9683661;
Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
Lehrach H., Hofer E., Francis F.;
"The genomic organization of NKG2C, E, F, and D receptor genes in the
human natural killer gene complex.";
Immunogenetics 48:163-173(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                     MEDLINE=91178434; PubMed=2007850;
Houchins J.P., Yabe T., McSherry C., Bach F.H.;
"DNA sequence analysis of NKG2, a family of related cDNA clones
encoding type II integral membrane proteins on human natural killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANTS ASN-2 AND PHE-102.
MEDLINE=21623889; PubMed=11751968;
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
Cleland S., Guechlein L.A., Uhrberg M., Parham P.;
"Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I-FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-I-SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
-I-SUBCELLULAR LOCATION: Type II membrane protein.
-I-TISSUE SPECIFICITY: Natural Killer cells.
-I-SIMILARITY: Contains 1 C-type lectin family domain.
Chordata, Craniata, Vertebrata, Buteleostomi, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR01304; Lectin_C.
Edm, PR00159; lectin_c; 1.
SMART; SM00034; CLBCT; 1.
PROSITE; PS00615; C_TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C_TYPE LECTIN 2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0004888; F:transmembrane receptor activity; TAS. GO; GO:0006968; P:cellular defense response; TAS. GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LONG FORM)
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BY SIMILARITY.
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EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                    Exp. Med. 173:1017-1020(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X54869; CAA38651.1; -.
EMBL; AA001684; CAA04922.1; -.
EMBL; Y13055; CAA33498.1; -.
EMBL; AF260134; AAF86972.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168:240-252(2002).
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DOMAIN 1 70
TRANSMEM 71 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; PT0374; PT0374.
Genew; HGNC:6375; KLRC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231
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                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE-Lymphoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biassoni R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKG2 genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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QVFLSEAFCWIGL---RNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQA--SSCE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 K--LVKSYHWMGLVHIPTNGSWQWEDGSILSPNLLTIIEMQKGDCALYASSFKGYIENCS 204
                                                                                                                                                                                                                                                                                                                      15 ATQAQNDYGPQQKS----SSSKPSCSCLVAITLG-----LLTAVLLSVLLYQWILCQ 62
                                                                                                                                                                                                                                                                                                                                                           31 STRCOKORCPVIKSKCRENASPLFFCCFIAVAMGIRFIIMVTIWSAVFLNSLFNOEVQIP 90
                                                                                                                                                                                                                                                                                                                                                                                               63 GSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLL
                                                                                                                                                                                                                                                                                                                                                                                                                      ---LIESYCGPCPKNWICYKENNCYQFFNESKNWYESQASCMSQNASLIKVYSKEDQDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS NKG2-A; NKG2-ADTM; NKG2-B AND NKG2-BDTM) MEDLINE-20322497; PubMed=10866118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9MZJ3; Q9MZJ8; Q9MZJ0; Q9MZJ1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94. -!- SUBCELLULAR LOCATION: Type II membrane protein. -!- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                 EXTRACELLULAR (POTENTIAL).

C.TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N.LINKED (GLCNAC. . .) (POTENTIAL).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            members and of NKG2-A,
                                                                                                                                                                                                                                             Length 216;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9MZJ3-4; Sequence=VSP 003065;
TISSUE SPECIFICITY: Natural killer cells.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                            A44883F31400DEAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification of novel transmembrane-deleted forms and D.";
                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                           Score 183.5; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LaBonte M.L., Levy D.B., Letvin N.L., "Characterization of rhesus monkey CD94/NKG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA
                                                                                                                                                                                                                                                                                   40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9MZJ3-2; Sequence=VSP_003064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=NKG2-Adtm;
IsoId=Q9MZJ3-3; Sequence=VSP_003063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lsoId=Q9MZJ3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 51:496-499(2000).
                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                 17.9%;
                                                                                                                                                                                                              25075
                                                                                                                                                                                                                                                                                       49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
                                       216
213
110
110
211
203
115
115
103
202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | : |
205 IPNTYIC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=NKG2-Bdtm;
                                       73
98
99
127
1189
115
131
202
216 AA;
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=NKG2-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=NKG2-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKGA MACMU
                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
                                                                                                                DISULFID
   TRANSMEM
                                                                                                                                       CARBOHYD
                                                                            DISULFID
                                                                                                  DISULFID
                                         DOMAIN
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                                                                                                                                                                                                                                                                                       Matches
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NKGA MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                    67 PPEKLTAEVLGIICIV-----LMATVLKTIVLIPFLEQNNSSPNTRTQKARHCGHCPEEW 121
                                                                                                                                                                                                                                                                                                                                                                     122 ITYSNSCYYIGKERRTWEESLLACTSKNSSLLSIDDEEEMKFLASILPSS--WIGVFRNS 179
                                                                                                                                                                                                                                                                                                                                              MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL-RNN 138
                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                     PQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCOGSNYST----CASCPDRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ပ
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenetics 51:496-499 (2000).
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HAA-E molecules by NK cells and some cytocoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- STSUE SPECIFICITY: Natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          warkt; bwu014; C TYPE LECTIN 2; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20322487; PubMed=10866118; LaBonte M.L., Levy D.B., Letvin N.L.; Mery E.B., Letvin N.L.; Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, and D.";
                                                                                                                                                                                                                                  14;
                         (POTENTIAL)
                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-D type_II integral membrane protein (NKG2-D activating NK
                                                                                                                                                                                                                                                                                                                                                                                                                          SGWRWEDGSPLNFSR--ISSNSFVQTCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 SHHPWVTINGLAFKHKIKDSDNAELNCAVLQVNRLKSAQCGSSMIYHCK 228
                                                                                                                                                                                            Length 231;
                                                          S -> N (in allele NKG2-C*02).
/FTIG4-VR 0119404.
S -> F (in allele NKG2-C*02).
/FTIG4-VAR_013405.
                                                                                                                                                                                                                                  76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                       -> I (IN REF. 1).
6B971EECD7542930 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
     N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                      Score 186; DB 1;
Pred. No. 1.2e-10;
                                             (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA
                                                                                                                                                                                                              Pred. No. 1.2e
31; Mismatches
                                           N-LINKED
S -> N (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF190943; AAF74539.1; -.
InterPro; IRRO1304; Lectin_C.
Pfam; PF00059; Dectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                           MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor) (NK cell receptor D)
                                                                                                                                                                                          ch 18.2%;
l Similarity 28.4%;
48; Conservative 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Polymorphism.
DOMAIN 1 51
                                                                                                                                                         26072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Macaca
       100
149
178
2
                                                                                                    102
                                                                                                                                           161
                                                                                                                                         161 1
231 AA;
                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=9544;
                                                                                                    102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKGD MACMU
                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                          139
       CARBOHYD
CARBOHYD
                                                                                                                                                                                                  Query Match
                                             CARBOHYD
                                                                VARIANT
                                                                                                      VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 STLTQKHNNSSLNTRTQKARHCGHCPEEWITYSNSCYYIGKEKRTWABSLLACTSKNSSL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVITDNOEMSLLOVFLSEAFCWIGL-RNNSGWRWEDGSPINFSR--ISSNSFVQTCGAIN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VIYSMLELPTATQAQNDYGPQQKSSSKPSCSC---LVAITLGLLTAVLL----SVLLYQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                    HSSP; P22897; IEGG.
InterPro; IPR001304; Lectin_C.
Fam; PF00059; Lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; P800615; C_TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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P26718; Q9NR41;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
NKG2-D type II integral membrane protein (NKG2-D activating NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLLSAPEKLIAGIIGIICLVLMASVVTIVVIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform NKG2-Bdtm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 183; DB 1; Length 233;
Pred. No. 2.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTEIN LINKED (GLCNAC. . .) (POTEIN LINKED) (GLCNAC. . .) (POTEIN LINKED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (In isoform NKG2-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (in isoform NKG2-Adtm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTId=VSP_003063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Alternative splicing.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Rischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mans G.I., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J. Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Brichards S., Mochey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rader J., Halton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. Brickey-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                              E, F, and D receptor genes in the
                                                                                                         MEDLINE=91178434; PubMed=2007850;
Houchins J.P., Yabe T., McBherry C., Bach F.H.;
Houchins J.P., Yabe T., McBherry C., a family of related cDNA clones
"DNA sequence analysis of NGZ, a family of related cDNA clones
encoding type II integral membrane proteins on human natural killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleland S., Guethlein L.A., Uhrberg M., Parham P.; "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  class I HIA-E molecules by NK cells and some cytotoxic T-cells.
-!-SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
-!-SUBCELLULAR LOCATION: Type II membrane protein.
-!-TISSUE SPECIFICITY: Natural Killer cells.
-!-SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kothapalli R., Kusmartseva I., Loughran T.P. Jr.; Identification and characterization of the NKG2D gene from large granular lymphocytic leukemia (LGL) cells "; Submitted (DEC-2011) to the EMBL/GenBank/DDBJ databases.
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT THR-72.
MEDLINE=21623889; PubMed=11/51968;
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
Cleland S., Guethlain L.A., Uhrberg M., Parham P.;
                                                                                                                                                                                                                                                                                 MEDLINE=98350122; PubMed=9683661; Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C., Lehrach H., Hofer E., Francis F.; "The genomic organization of NKG2C, E, F, and D receptor gent human natural killer gene complex."; Immunogenetics 48:163-173(1998).
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                           J. Exp. Med. 173:1017-1020(1991)
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Bukaryota; Metazoa;
                         Mammalia; Eutheria;
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EMBL; X54870; CAA38652.1; -.

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PIR; 154524; 154524.
HSSP; P05451; 1LIT.
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                                                                                                                                                                                                                                                   GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001364; Lectin_C.
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
SMOSTIE; PS00611; CLECT; 1.
PROSTIE; PS00611; C_TYPE_LECTIN 1; FALSE_NEG.
PROSTIE; PS50041; C_TYPE_LECTIN 2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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01-N0V-1997 (Rel. 35, Created)
01-N0V-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-E type II integral membrane protein (NKG2-E activating l
receptor) (NK cell receptor B).
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SEQUENCE FROM N.A. (ISOFORM NKG2-E).
MEDLINE=94102823; PubMed=8276468;
Adamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;
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C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
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J. AJ001687; CAA04925.1; --
J. AJ001689; CAA04925.1; JOINED.
J. AJ001689; CAA0425.1; JOINED.
J. AF461811; AAL65233.1; --
J. AF260135; AAF86973.1; --
J. AF260135; AAF86973.1; --
J. AF260136; AAF86973.1; --
J. BC039836; AAH39836.1; --
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26.8%;
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                                                                                                                                                                              PT0375; PT0375.
1HYR; 23-MAY-01.
1KCG; 09-JAN-02.
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EMBL;
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PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 602892; -. 602004898; Fitransmembrane receptor activity; TAS. 60;0004889; Fitransmembrane receptor activity; TAS. 60;0006568; P:cellular defense response; TAS. InterPro; IPR001304; Lectin_C. Fam: PF00059; lectin_c; 1. Fam: PF00059; lectin_c; 1. Fam: PF00059; lectin_c; 1. FROSITE; PS00041; C_TYPE_LECTIN_1; FALSE_NEG. FROSITE; PS50041; C_TYPE_LECTIN_2; 1. FROSITE; PS50041; C_TYPE_LECTIN_2; 1. FROSITE; PS50041; C_TYPE_LECTIN_2; 1. FROMENTAL). CTYPELASMIC (POTENTIAL). TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C., Lehrach H., Hofer B., Francis F., "The genomic organization of NKG2C, B, F, and D receptor genes in the human natural killer gene complex.";
"Natural killer lectin-like receptors have divergent carboxy-termini, distinct from C-type lectins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P.; "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i-FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytocoxic T-cells. -i-SUBURIT: Can form disulfide-bonded heterodimer with CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99218418; PubMed=10201920; Bellon T., Heredia A.B., Llano M., Minguela A., Rodriguez A., Bellon T., Heredia A.B., Llano M., Minguela A., Rodriguez A., Lropez-Botet M., Aparicio D.; "Triggering of effector functions on a CD8+ T cell clone upon the aggregation of an activatory CD94/kp39 heterodimer."; J. Immunol. 162:3996-4002(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM NKG2-E), AND VARIANT ARG-19.
MEDLINE=21623889; Pubmed=11751968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isold=007444-2; Sequence=VSP 003067;
-!- TISSUE SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).

EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q07444-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM NKG2-H).
                                                                                                                                                                                         FROM N.A. (ISOFORM NKG2-E)
                                                                                                                                                                                                                        MEDLINE=98350122; PubMed=9683661;
                                                                         distinct from C-type lectins.";
Immunogenetics 39:218-218(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, L14542; AAA16833.1; -.
EMBL, AJO01685; CAA04923.1; -.
EMBL, AF078550; AAD46108.1; -.
EMBL, AF350016; AAK83803.1; -.
EMBL, AF350017; AAK83804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKG2 genes.";
J. Immunol. 168:240-252(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:6376; KLRC3.
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DISULFID
DISULFID
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us-09-811-367b-1.open.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN-QEMSLLQVFLSEAFCWIGL-RN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 PQOKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYST----CASCPSCPDRW 79
                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
RRGFIMLTRLVLNS -> VSISFRIKALELAVHQIKFYICS
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE=21623889; PubMed=11751968;
Shum B.P., Flodin L.R., Muir. D.G., Rajalingam R., Khakoo S.I.,
Cleland S., Guechlein L.A., Uhrberg M., Parham P.;
"Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKG2 genes.";
J. Immunol. 168:240-252(2002).
J. Immunol. 168:240-252(2002).
J. Immunol. 168:240-252(2002).
J. Immunol. 168:240-252(2002).
J. SUBCHILLS HAA-E molecules by NK cells and some cytotoxic T-cells.
J. SUBCHILLOLAR LOCATION: Type II membrane protein.
J. SUBCELINIAR LOCATION: Type II membrane protein.
J. TISSUE SPECIPICITY: Natural killer cells.
J. SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                          15;
        (GLCNAC. . .) (POTENTIAL)
                                .) (POTENTIAL)
.) (POTENTIAL)
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-E type II integral membrane protein (NKG2-E activating NK
                                                                                                           NRNDIMIA (in isoform NKG2-H).
/FTId=VSP_003067.
P -> R (in allele NKG2-E*02).
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                                                                                                                                                                                                                                                                                                                                                                                                             70; Indels
                                                                                                                                                                                               /FTId=VAR_013296.
R -> S (in dbSNP:1138437).
/FTId=VAR_014660.
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                                                                                                                                                                                                                                                                                         20691FB21274D8A6 CRC64;
                          N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
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EMBL, AF350007, AAK83794.1; -.
InterPro; IRR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PRART; SM00034; CIECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                               Score 178.5;
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179
227
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095MI4; 095MI3;
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  CARBOHYD
                          CARBOHYD
                                                        CARBOHYD
                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                    VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :| :: | :| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN-QEMSLLQVFLSEAFCWIGLRNN 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POOKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYST----CASCPSCPDRW
                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Natural killer cell surface protein Pl-3.2.3 (NKR-Pl 3.2.3) (Antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90378305; PubMed=2399464;
Giorda R., Rudert W.A., Vavassori C., Chambers W.H.,
Hiserodt J.C., Trucco M.;
"NKR-Pl, a signal transduction molecule on natural killer cells.";
Science 249:1298-1300(1990).
Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 249:1296-1300(1990).

-!- FUNCTION: Mediates transmembrane signaling in natural killer (RIX) cells and so may act as a receptor able to selectively trigger NK cell activity.

-!- SUBGNIT: Homodimer.

-!- SUBCELLULAR LOCATION: Type II membrane protein.

-!- TISSUE SPECIFICITY: Natural killer cells.

-!- MISCELLANBOUS: Ligand binding may be calcium dependent.

-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 240;
                                                                                                            (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

C -> R (IN NKG2-E+02).

C -> R (IN NKG2-E+02).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :| :| : | : | SSHHPWVIINGLAFKHBIKDSDHAERNCAMLHVCGLISDQC 220
                                                                                                                                                                                                                                                                                                                                17.4%; Score 177.5; DB 1;
28.0%; Pred. No. 7.9e-10;
Nismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AA
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HSSP; P22897; IEGG.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
                                                                                                                                                                                                                                                                                                    26996 MW:
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                     Glycoprotein; Polymorphism.
1 70
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128
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Local Sim
   Receptor;
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                                                                                    TRANSMEM
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75 -CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVF---LSEAF 130
                                                                                                                                                                                                                                                   93 KCPKDWLSHRDKCFHVSQTSITWKESLADCGGKGATLLLVQDQEELRFLRNLTKRISSSF 152
                                                                                                                                                                                                                                                                            131 CWIGLR---NNSGWRWEDGSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                       24 POOKSSSKRPSCSCLVAITLGLL-TAVLLSVLLYQ-----WILCQGSNYSTCASCPS-- 74
                                                                                                                                                                                                              35 PRSHRLALKLSCAGLILLVLALVGMSILVRVLVQKPSVEPCRVLIQ-ENLSKTGS-PAKL 92
                                                                                                                                                              Query Match 17.2%; Score 175.5; DB 1; Length 223; Best Local Similarity 27.1%; Pred. No. 1.1e-09; Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

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August 10, 2004, 16:05:01; Search time 46.8319 Seconds (without alignments) 1140.281 Million cell updates/sec

US-09-811-367B-1

1023 1 WIDSVIYSMLELPTATQAQN.....GLQASSCEVPLHGVCKKVRL 189 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

ritle:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

STIMMARTES

	Description	Aaw88265 Human mas	9 Human ma	Bindin	١.	Mouse	3 Mammal		Rat	Huma			Human		Human	Human	Human		Human	Human	Aam14192 Peptide #		Aam26602 Pentide #	Human		Human
SUMMARIES	ID	AAW88265	AAE11759	ADD25635	ABG05451	AAE11760	AAR77033	AAW88277	AAE11761	AAW88267	AAR77472	AAW88266	ABB81897	AAM88815	AAU19820	ABP48040	ADC11002	AAU19659	ABP47879	ADC10841	AAM14192	ABB33139	AAM26602	ABB27967	ABB18604	AAM66323
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	Length	189	189	æ	843	188	188	188	188	66	114	7.0	231	198	198	198	198	203	203	203	35	35	35	35	35	32
ok	Query Match	100.0	100.0	98.4	77.1	53.6	51.4	51.4	51.4	42.1	36.2	30.0	22.5	22.1	22.1	22.1	22.1	22.1	22.1	22.1	21.2	21.2	21.2	21.2	21.2	21.2
	Score	1023	1023	1007	789	548.5	525.5	525.5	525.5	431	370.5	306.5	230	226	226	226	226	226	226	226	217	217	217	217	217	217
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Aam53935 Human bra				Human	Human					Aaw40222 CD94, 7/1	Human	Murine		Aab85871 0. cunicu			_	Aar99586 Low densi	Aay24152 Bovine LD
AAM53935	ABG47989	AAM01928	ABG35971	AAU19660	ABP47880	ADC10842	AAR65189	AAB68584	AAW64791	AAW40222	ADE76965	AAR54660	AAW85595	AAB85871	ABJ19328	AAE37769	AAW85594	AAR99586	AAY24152
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21.2	21.2	21.2	21.2	21.2	21.2	21.2	19.6	19.3	19.2	19.2	19.2	19.2	19.2	19.1	19.0	19.0	18.9	18.9	18.9
217	217	217	217	216.5	216.5	216.5	201	197	196.5	196.5	196.5	196.5	196.5	195.5	194	194	193	193	193
26	27	28	29	30	31	32	33	34	35	36	37	38	33	40	4.	42	43	44	45

ALIGNMENTS

Mast cell function-associated antigen; MAPA; splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy. Human mast cell function-associated antigen (MAFA). Lamers MBAC, Lamont A, Williams DH; 137. .139 /note= "Asn is N-glycosylated" 150. .152 /note= "Asn is N-glycosylated" "Asn is N-glycosylated" /note= "Asn is N-glycosylated" Location/Qualifiers 7. .10 /note= "ITIM motif" AAW88265 standard; protein; 189 AA (PEPT-) PEPTIDE THERAPEUTICS LID 97GB-00011148. 98WO-GB001572, 29-MAR-1999 (first entry) 65. .67 /note= "} 66. Modified-site Modified-site Modified-site Modified-site Homo sapiens WO9854209-A2 29-MAY-1998; 31-MAY-1997; 03-DEC-1998, Hewitt EL, AAW88265; Key Peptide AAW88265

New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth. WPI; 1999-059806/05. N-PSDB; AAV84198.

Disclosure, Fig 1, 44pp, English.

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This is the amino acid sequence of human mast cell function- associated antigen (MAFA), a type II membrane glycoprotein. CDNA (see AAV84198) encoding human MAFA can be obtained from myelogenous leukaemic cell line KUB12 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW8827) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2 Alternatively spliced forms (see AAW88266-67) of human MAFA have been identified. Polypeptides and synthetic peptides (see AAW88258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pharmaceutical composition, mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                   CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
                                                                                                                                                                                                                                                                                                                                                          MTDSVIYSMLELPIATQAQNDYGPQQKSSSSKPSCSCLVAITLGLITAVLLSVLLYQWIL
                                                                                                                                                                                                                                                                                                                               MIDSVIYSMLELPIATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                           Length 189;
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                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                         100.0%; Score 1023; DB 2;
100.0%; Pred. No. 1.8e-98;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-2000; 2000US-0190716P.
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                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 189; Conservative
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                                                                                                                                                                                                                              Sequence 189 AA;
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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell. by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition or the subject, to NK or T-cell or the target cell expressed celled; tinn amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating on the target cell. The agent or the composition is useful for treating or tumour by stimulating the cyctoxic activity of an NK cell or a cytocoxic T-cell (CTL), where the tumour comprises an NK cell- or a cytocoxic tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is human MAFA protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidabetic; antithyroid; anteroprotective; hinge region; immunoglobulin heavy chain; cH2 constant region; CH3 constant region; CH3 constant region; GH3 constant region; GH3 constant antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent call-mediated cytotoxicity; ADCC; complement fixation; rheumatoid arthritis; myaethenia gravis; Grave's disease; rheumatoid arthritis; myaethenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                       Length 189;
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                                                                                                                                                                                                                                                                                                                                                                            DB 4;
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Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1023; 100.0%; Pred. No. 1.
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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Ledbetter JA,

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comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide.

CC funge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, amutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more expective residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more expective residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains

CC apparent residue; and a mutated human IgG1 immunoglobulin fusion protein is capable of at least one immunoglobulin hinge region protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antidem. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polymucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein, a recombinant or polymucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell assublet having or suspected of having a malignant condition or a B-cell New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease. The invention relates to a binding domain-immunoglobulin fusion protein Disclosure; SEQ ID NO 196; 157pp; English.

Sequence 189 AA;

disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at

segdata uspto gov/sequence.html?DooID=2033118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

0 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120 121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSRPSCSCLVAIALGLLTAVLLSVLLYQWIL 60 CQGSNYSICASCPSCPDFWWKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS . 0 98.4%; Score 1007; DB 7; Length 189; 98.4%; Pred. No. 8.5e-97; ive 1; Mismatches 2; Indels (Best Local Similarity 98.4 Matches 186; Conservative HGVCKKVRL 61 61 181 Query Match 121 셤 임 ద à δ à

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. Novel human diagnostic protein #5442. ABG05451 standard; protein; 843 AA. 30-MAR-2001; 2001WO-US008631. Tang YT; 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167 (first entry) Drmanac RT, Liu C, WPI; 2001-639362/73. (HYSE-) HYSEQ INC. N-PSDB; AAS69638 WO200175067-A2. biodiversity. Homo sapiens. 13-FEB-2002 11-OCT-2001 ABG05451; ABG05451

Claim 20; SEQ ID NO 35810; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to reserve normal carivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations capponable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and mind amino acid sequences have and products dependent on DNA and mind amino acid sequences the context diagnostic and to produce other types of data and products dependent on DNA and mind amino acid sequences. amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published pct sequences

Sequence 843 AA;

0; 130 724 11 ELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYSTCA 565 ELPTATÓAQNDYGPQQKSSSRPSCSCLVAIALGLLTAVLLSVLLYQWILCQGSNYSTCA SCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAF 0; Length 843; Indels Score 789; DB 4; L Pred. No. 3.7e-73; 8; Mismatches 8; 77.18; 89.98; 143; Conservative Local Similarity 71 Query Match Matches

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181 HWVCKKVRL 189

RESULT

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CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guthmann MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-366356/47.
                                                                                                                                                                                        180 QWICKKV 186
                                                                                                                                                     181 HGVCKKV 187
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Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural Killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition on the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic common comprises an NK cell or TI-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is mouse MAFA protein
                                                                                                                                                                                                                                                                                                  Mouse; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
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                                                                                                                                                                                                                                                                     Mouse mast cell function associated antigen (MAFA) protein.
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                       CWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKN 169
                                             CWIGLRNNSGWRWEDGSPLNFSRNTNGTIIRKRKHLHKN 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%; Score 548.5; DB 4;
55.6%; Pred. No. 6.7e-49;
iive 26; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                        64. .188
/note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                       AAE11760 standard; protein; 188 AA
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                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi N, Mikayama T;
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                                                                                                                                                                                          AAE11760;
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1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLITVILMSLLMYQRIL 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL

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61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEBKDWNSSLEFCLARDSHLLVITDNQEMS 120
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CCGSKDSTCSHCPSCPILM_TRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLITFPDNQGVK 120
                                                                                   LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                      Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            combination with the MAFA to prevent inflammatory and allergic reactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A soluble form of mast cell function-associated antigen (MAFA) can k produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalian mast cell function-associated antigen (MAFA).
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53.5%; Pred. No. 1.7e-46;
iive 29; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAR77033 standard; protein; 188 AA
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LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL

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New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic
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                                                                                                                                                                                                            Mast cell function-associated antigen, MAPA, splice variant, rat, inflammation; allergy, asthma, rheumatoid arthritis; tumour; therapy.
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                                                                                                                                                                                 Rat mast cell function-associated antigen (MAFA).
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                                                                                                                                                                                                                                                                                                             "Asn is N-glycosylated"
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                                                                                              AAW88277 standard; protein; 188 AA
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                                                                                                                                                      (first entry)
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Best Local Similarity 53.5'
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                82. .84
/note= "
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181 HGVCKKV 187
                          180 QWICEKV 186
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                                                                                                                                                      29-MAR-1999
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CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120 CGGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFFPDNGGVN 120

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1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60

Gaps ij

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The present invention relates to a pharmaceutical composition comprising antigen (WAPA) ligand on a target cell, and prevents or inhibite natural killer (NR) or T-cell-expressed cell surface MAPA from binding to MAPA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NR- or a T-cell-expressed cell surface MAPA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition on the target cell. The agent or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAPA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or creating tumour by stimulating the cytotoxic activity of an NK cell or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
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                                                                                                                                                                                                                                                                                     Rat; pharmaceutical composition, mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MAFA protein
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                                                                                                                                     AAE11761 standard; protein; 188 AA.
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                                                                                                                                                                                                            (first entry)
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                                       186
   181 HGVCKKV 187
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Best Local Similarity
Matches 100; Conserv
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QWICEKV
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75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
           121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                 Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergy; allergic;
                               ---ISSNSFVQTCGAITKNGLQASSCEVPL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel DNA encoding a mast cell function-associated antigen (WAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
                                                                                                                                                                                                                                                         Partial sequence of mast cell function-associated antigen (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 36.2%; Score 370.5; DB 2
1 Similarity 58.4%; Pred. No. 1.4e-30;
66; Conservative 18; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 38; 54pp; English.
                                                                                                                                                                        AAR77472 standard; protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW88266 standard; protein; 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tal M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            94IL-00109257.
                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US004258.
                                                                                                                                                                                                                                (first entry)
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                                                                                                HWVCKKVRL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-366356/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 66; Conserv
                                                                       181 HGVCKKVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT01471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES
(RYCU/) RYCUS A.
                                                                                                                                                                                                                                                                                                                                                Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                          W09527734-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1994;
                                                                                                                                                                                                                                01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                     19-0CT-1995
                                                                                                                                                                                                                                                                                                                prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW88266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pecht I,
                                           64
                                                                                                   91
                                                                                                                                                                                                    AAR77472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to human mast cell
and manufacturing
inflammatory and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                              9
                                            LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of human mast cell function- associated antigen (MAFA) splice variant huMAFA(B3/4-), which lacks the C-lectin-like domain of human MAFA (see AAM88265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail. Truncated MAFA polypeptides including huMAFA(B3/4-), and polymucleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIDSVIYSMLELPTATQAQNDYGPQQKSSSSRPSCSCLVAIALGLLTAVLLSVLLYQWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTDSVIYSMLELPTATOAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
CGGSKGFMCSQCSRCPNIMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLITFPDNQGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                                                                                  Mast cell function-associated antigen, MAFA, huMAFA(E3/4-); splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 431; DB 2; Length 99;
Pred. No. 5.4e-37;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide having a sequence corresponding function-associated antigen - useful in forming pharmaceutical compositions in the treatment of
                                                                                                                                                                                                                                                                                         Human MAFA splice variant huMAFA(E3/4-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lamont A,
                                                                                                                                                                                                       AAW88267 standard; protein; 99 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEPT-) PEPTIDE THERAPEUTICS LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97GB-00011148.
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50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases, and tumour growth
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lamers MBAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95; Conservative
                                                                                                      181 HGVCKKV 187
                                                                                                                               QWICERY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-059806/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 99 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1997;
                                                                                                                                                                                                                                                              29-MAR-1999
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                                                                                                                                                                                                                                   AAW88267;
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                                              121
                                                                                                                               180
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P
                                                                                                                                                                                                                                                                                                                                                                                                                                    intracellular and transmembrane regions of human MARA (see AAM88265), followed immediately by a polyproline motif (see AAM88264) due to a reading frameshift. This unique motif has been used to design peptides (see AAW8829-64, AAW88268-72) that inhibit T cell antigen receptor-dependent activation induced by interleukin-2 (IL2) secretion from human Jurkat T cells or IgE dependent degranulation of rat basophil leukaemic cells. Inhibition of IL2 production prevents T cell proliferation and suppresses the immune system. These peptides, truncated MARA polypeptides including huMAFA(E3-), and polynucleotides encoding them, can be used in compositions for the treatment of inflammatory and allergic
                                                                                                                                                                                                                                                                                                        New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.
                                                        sll function-associated antigen; MAFA; huMAFA(E3-); splice variant;
inflammation; allergy; asthma; rheumatoid arthritis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIDSVIYSMLELPTATQAQNDYGPQQKSSSRPSCSCLVAIALGLLTAVLLSVLLYQMIL 60
                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of human mast cell function- associated
                                                                                                                                                                                                                                                                                                                                                                                                   antigen (MAFA) splice variant huMAFA(E3-). huMAFA(E3-) is a major transcript, not found in rat, but highly expressed in human lung and granulocyte-enriched blood cells. The truncated protein includes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases (e.g. rheumatoid arthritis and asthma), or tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                Williams DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%; Score 306.5; DB 2;
82.9%; Pred. No. 3.5e-24;
iive 1; Mismatches 5;
                                 Human MAFA splice variant huMAFA(E3-)
                                                                                                                                                                                                                                                Lamont A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB81897 standard; protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 2; 44pp; English.
                                                                                                                                                                                                                        (PEPT-) PEPTIDE THERAPEUTICS LTD
                                                                                                                                                                                                 97GB-00011148.
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         (first entry)
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                                                                                                                                                                                                                                                Lamers MBAC,
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                                                                                                                                                                                                                                                                       WPI; 1999-059806/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 63; Conserv
                                                                                                                                                                                                                                                                                  N-PSDB; AAV84199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 70 AA;
                                                                                                       Homo sapiens.
         29-MAR-1999
                                                                                                                              WO9854209-A2
                                                                                                                                                                          29-MAY-1998;
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                                                                                                                                                                                                                                                EL,
                                                        Mast cell
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                                                                                 therapy.
                                                                                                                                                                                                                                                Hewitt
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Matches
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New NKp80 polypeptides having a triggering NK activity, useful as markers for typing lymphoproliferative diseases of granular lymphocytes, or for identifying abnormal cells in the whole lymphocyte population in patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GLLTAVLLSVLLY----QWILCQG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to a novel human polypeptide (designated NKp80)
Human; NKp80; triggering NK; lymphoproliferative diseases; LDGL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 231;
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                                                                                                                                                                                                                                               /note= "Encoded by ACA"
                                                                                                                                                                                            'note= "Encoded by CAA"
                                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by ATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 1; 21pp; English.
                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                     note= "Encoded"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INNA-) INNATE PHARMA
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N-PSDB; ABQ78832.
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ses 63; Conserv
                                                                                                                                                                                                                                                                         Misc-difference 64
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                                                                                  Homo sapiens
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                               lymphocyte.
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2000US-0232398P.
2000US-0232399P.
2000US-0232401P.
2000US-0233063P.
2000US-0233063P.
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2000US - 023424P.
2000US - 023499P.
2000US - 023499P.
2000US - 023584P.
2000US - 0235834P.
2000US - 0235836P.
2000US - 023636P.
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2000US-0237039P.
2000US-0237040P.
2000US-0239935P.
2000US-0249960P.
2000US-024178FP.
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2000US-0244617P.
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   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                          Human immune/haematopoietic antigen SEQ ID NO:16408
                              AAM88815 standard; protein; 198 AA
                                                                                                                                                                                                                                                                                                                                         04-FEB-2000; 2000US-0180648P.
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                                                             AAM88815;
 RESULT 13
                AAM88815
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Human novel extracellular matrix protein, Seg ID No 470.
  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially cancer metastases of haematopoietic-derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQTVLCQSEWLKYQGKCYWFSNEMKSWSDSYVYCLERKSHLLIHDQLEMAFIQKNLRQL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -FCWIGLRNNS---GWRWEDGSPLNFSRISSNSFVQ-----TCGAINKNGLQASSCEVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK84764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAW62169 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 16408; 3071pp + Sequence Listing; English.
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06-DEC-2000; 2000US-025149P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251969P.
08-DEC-2000; 2000US-025199P.
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                                                                                                                                                    (HUMA-) HUMAN GENOME
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immunomodulatory; Anti-HIV;
Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial, ophthalmic; oytostatic; antialzabiemers; immune/automimune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; sezary syndrome; disease; neurological diseases; Alzheimer's disease; parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
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human secreted extracellular matrix proteins (SPs). The polynucleotides can divident secreted extracellular matrix proteins (SPs). The polynucleotides can and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and probe in diagnostic assays. The SPs may also be used as INA probe in diagnostic assays. The SPs may also be used as INA produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumacoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of diseases (e.g. Altheimer's disease, parkinson's disease), neurological (c. the breast or liver, Sezary syndrome and Gaucher's disease), neurological (c. the breast or liver, Sezary syndrome and Gaucher's disease), neurological (c. the breast or liver, Sezary syndrome and Gaucher's disease), neurological (c. the breast or liver; disease, parkinson's disease) cardio-(ceretions caused by bacteria, viruses and thugi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of of organs before transplantation, support of cell culture of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 ----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLQVFLSEA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
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31.2%; Pred. No. 3.5e-15;
iive 27; Mismatches 53; Indels 48; Gaps
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                                          05-DEC-2000; 2000US-0256719P.

06-DEC-2000; 2000US-0251479P.

08-DEC-2000; 2000US-0251866P.

08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-025199P.

08-DEC-2000; 2000US-025199P.

11-DEC-2000; 2000US-025199P.
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Best Local Similarity 31.24
Matches 58; Conservative
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ABP48040 standard; protein; 198 AA.

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immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antithemmatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiocorvisant; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                         Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                   Human polypeptide SEQ ID NO 470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-2000; 2000US-0229513P.
08-SEP-2000; 2000US-0231413P.
21-SEP-2000; 2000US-0234223P.
21-SEP-2000; 2000US-0234223P.
25-SRP-2000;
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11-JUL-2000; 2000US-0217496P.
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                               (first entry)
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14-AUG-2000;
14-AUG-2000;
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20-OCT-2000;
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                              23-AUG-2002
          ABP48040;
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The invention relates to novel genes (ABQ66521-ABQ66785) and proteins (ABP47846-ABP48110) useful for preventing, treating or ameliorating conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancers do the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune concerns actions of the adversal and the actions of the actions and ulcertive colitis; (c) anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcertive colitis; (c) ardiovascular disorders e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly communication of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                               New nucleic acid encoding human proteins, useful for diagnosis, treatment and prevention of e.g. osteoporosis, also related polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
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N-PSDB; ABQ66715.
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OM protein - protein search, using sw model

August 10, 2004, 16:18:53; Search time 40.4761 Seconds (without alignments) 1464.718 Million cell updates/sec Run on:

Perfect score:

US-09-811-367B-1 1023 1 MTDSVIYSMLELPTATQAQN......GLQASSCEVPLHGVCKKVRL 189 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1291235 seqs, 313682936 residues Searched:

1291235 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:*

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			Description	Sequence 1, Appli	Sequence 196, App	Sequence 3, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 470, App	Sequence 470, App	Sequence 309, App	Sequence 309, App	Sequence 33902, A	Sequence 310, App	Sequence 310, App	Sequence 25. Appl	Sequence 130. App	Sequence 10, Appl	
Committee			ID	US-09-811-367B-1	US-10-207-655-196	US-09-811-367B-3	US-09-811-367B-5	US-10-451-843-1	US-09-764-870-470	US-10-125-540-470	US-09-764-870-309	US-10-125-540-309	US-09-864-761-33902	US-09-764-870-310	US-10-125-540-310	US-10-379-127-25	US-09-919-039-130	US-10-335-009-10	
				6	14	σ	σ	16	σ	14	σ	14	9	σ	1.4	15	10	15	
			Match Length DB	1.89	189	188	188	231	198	198	203	203	35	182	182	225	179	179	
	₩	Query	Match	100.0	98.4	53.6	51.4	22.5	22.1	22.1	22.1	22.1	21.2	21.2	21.2	19.6	19.2	19.2	
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Sequence 7, Appli Sequence 11, Appl Sequence 22, Appl Sequence 25, Appl Sequence 25, Appl	304, 44, 100, 100, 100, 100, 100, 100, 10	Sequence 2, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appl Sequence 11, Appl Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli
14 US-10-179-528-7 14 US-10-220-511-11 15 US-10-161-493-22 18-10-161-493-22 14 US-10-179-528-4	US-10-220-511 US-09-764-870- US-10-125-870- US-10-161-493 US-10-161-493 US-10-451-459 US-10-138-588 US-10-138-588 US-10-220-511 US-10-220-511 US-10-276-774 US-09-862-888 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774 US-10-276-774	14 US-10-11-27-47-2 14 US-10-184-150-1 15 US-10-369-214-131 15 US-10-328-997-1 10 US-02-284-320-11 13 US-10-114-893-32 14 US-10-179-528-1
199 278 268 226 257	222 202 202 202 202 203 203 204 204 204 204 204 204 204 204 204 204	4 4 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
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16 11 19 20	12 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

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APPLICANT: GEMINI SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACETTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THER FILE REFERENCE: 201286/027819
CURRENT APPLICATION NUMBER: 20/9/911,367B
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 20
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; Pred. No. 3.5e-97;
0; Mismatches 0;
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Patent No. US20020155110A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 189; Conservative
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ORGANISM: Homo sapiens
JS-09-811-367B-1
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GENERAL INFORMATION:
APPLICANT: GENINIS SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US2020155110Aluaki
APPLICANT: Mikayama, Toshifumi
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
FILE REPERENCE: 021286/0278719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-451-843-1

Sequence 1, Application US/10451843

Sequence 1, Application Vo. US20040115738A1

Publication No. US20040115738A1

GENERAL INCAME PHARMA S.A.S.

APPLICANT: UNIVERSITA DI GENOVA

TITLE OF INVENTION: Polypeptides having a triggering NK receptor activity and biolog

TITLE OF INVENTION: applications

FILE REFRENCES: 1249MKR80

CURRENT APPLICANTON NUMBER: US/10/451,843

CURRENT FILING DATE: 2003-12-30
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                                                                                                                    61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
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Best Local Similarity 53.5%; Pred. No. 6.7e-46;
Matches 100; Conservative 29; Mismatches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5, Application US/09811367B; Patent No. US20020155110A1
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Batent No. US20020155110A1

GENERAL INFORMATION:

APPLICANT: GEMINI SCIENCE, INC.

APPLICANT: ARABABBI, No. US20020155110A1uaki

APPLICANT: Mikayama, Toshifumi

TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)

TITLE OF INVENTION: PHARMACETICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM FILE REFERENCE: 021286/0278719

CURRENT APPLICATION NUMBER: US/09/811,367B

PRIOR FILING DATE: 2002-03-12

PRIOR PRIOR APPLICATION NUMBER: 60/190,716
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                                                                                                                                                                         Sequence 196, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledberter, Jeffrey A.
APPLICANT: Ledberter, Jeffrey A.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNOSICOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-4010.
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 196
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Pred. No. 1.6e-95;
1; Mismatches 2; Indels 0
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55.6%; Pred. No. 2.9e-48;
iive 26; Mismatches 56;
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98.4%;
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 55.65
Matches 104; Conservative
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Best Local Similarity 98.4<sup>5</sup>
Matches 186; Conservative
                             HGVCKKVRL 189
                                                                      HGVCKKVRL 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                      15 KKRSSAQTSCLTFKDYSVTLHWYKILLGISGTVNGILTLTLISLILLVSCGVLLKCQKGS 74
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                                                                                                                                                      Length 231;
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Fatent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
FAILO application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIN Ver. 2.0
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                                                                                                                                                                                              61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SKIFFIKGPAKENSCAAIKESKIFSETCSSVFKWICQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRISSNSFVQ-----TCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                    ch 22.5%; Score 230; DB 16; Score 230; DB 16; Similarity 28.6%; Pred. No. 2.5e-15; 63; Conservative 32; Mismatches 61;
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78-10-125-540-470
; Sequence 470, Application US/10125540
; Publication No. US20030059875A1
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                                                                                                                                                                                                                                  26 QKSSSSKPSCSCL--VAITL-
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
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ORGANISM: Homo sapiens
US-09-764-870-470
                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-764-870-470
                                      SEQ ID NO 1
LENGTH: 231
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US-10-451-843-1
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LENGTH: 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 -FCWIGLRNNS---GWRWEDGSPLNFSRISSNSFVQ-----TCGAINKNGLQASSCEVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 ----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLQVFLSEA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SNYSTCASCPS
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                                                                                                                                                                                                                                                                                                                                        Length 198;
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Patent No. US20020042386A1

GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REBERENCE: PTZ14

CURRENT APPLICATION NUMBER: US/09/764,870

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
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22.1%; Score 226; DB 14;
Best Local Similarity 31.2%; Pred. No. 5.4e-15;
Matches 58; Conservative 27; Mismatches 53;
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31.2%; Pred. No. 5.5e-15;
tive 27; Mismatches 53
                                                                                                                   Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 646
SOFFWARE PatentIn Ver. 2.0
SEQ ID NO 470
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 GLLTAVLLSVLLY--QWIL--CQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                44 GLLTAVLLSVLLY--QWIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 309
LENGTH: 203
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                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 FKWICQ 197
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Best Local Similarity
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Gaps
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NH: EXPRESSED IN BAT474, SIGNAL = 8.9

NH: EXPRESSED IN BAT6, SIGNAL = 6.3

NH: EXPRESSED IN HEART, SIGNAL = 6.3

NH: EXPRESSED IN PLACENTA, SIGNAL = 18

NH: EXPRESSED IN PLACENTA, SIGNAL = 18

NH: EXPRESSED IN PLACENTA, SIGNAL = 22

NH: EXPRESSED IN HELA, SIGNAL = 13

NH: EXPRESSED IN HELA, SIGNAL = 13

NH: EXPRESSED IN HELA, SIGNAL = 6.1

NH: EXPRESSED IN HELLO, SIGNAL = 6.1

NH: EXT HUMAN HIT: AAL88327.1, EVALUE 1.00e-14

NH: SWISSPROT HIT: P14370, EVALUE 3.00e-04
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Patent No. US20020042386A1;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLEic Acids, Proteins, and Antibodies;
FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764.870
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper;
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
SEQ ID NO 310
SEQ ID NO 310
SED INGTH: 182
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: DCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 33302
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100.0%; Pred. No. 5.3e-15;
cive 0; Mismatches 0;
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Pred. No. 4.6e-14;
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35.0%;
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Best Local Similarity 100.0
Matches 35; Conservative
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CRGANISM: Homo sapiens
US-09-764-870-310
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Best Local Similarity
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US-09-764-870-310
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 DQTVLCQSEWLKYQGKCYWFSNEWKSWSDSYVYCLERKSHLLIIHDQLEMAFIQKNLRQL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 -----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Indels
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFERENCE: PT214C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT APPLICATION NUMBER: US/204-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 GLLTAVLLSVLLY -- OWIL -- CQG---
                                                                                                                                                        Sequence 309, Application US/10125540 Publication No. US20030059875A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Conservative
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ORGANISM: Homo sapiens
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               197 FKWICQ 202
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Best Local Similarity
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                                                                                              RESULT 9
US-10-125-540-309
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APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: CENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: US/09/919,039
PRIOR APPLICATION NUMBER: 06/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFFWARE: PROGram
SEQ ID NO 130
                                                                                     8
                                                                                                                                                                                                                                                                                              91 VEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145
                                                                                                                                                                                                                                                                                                                        54 VVTGLSVSVT----SLIQKSSIEKCSVDIQQSRNKTTERPGLINCPIYWQQLREKCLLFS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 OKTWNESRHLCASOKSSLLOLONTDELDFMS--SSQOFYWIGLSYSEEHTAWLWENGSAL 136
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                                                                                                                          SCSCLVAITLG
                                                                                                                                                                 1 MDQQAİYAELNLPİ-----DSGPESSPSSLPRDVCQGSPWHQFALKLSCAGIILLVL-
                                                                                                                                                                                                             -SCPSCPDRWMKYGNHCYYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL
                                                                                     Gaps
                                                                                  48;
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PSPLICANT: Boles, Kent S.
TITLE OF INVENTION: LLT USS THEREOF IN IMMUNE SYSTEM MODULATION
FILE REFERENCE: 11707.02/469687-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 179;
                                       Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                         | | | | : : | : : | : | : | : | 170 GSFLNSNDLEIRGDAKENSCISISQTSVYSBYCSTBIRWICQK 212
                                                                                                                                                                                                                                                                                                                                                                              146 GSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SQYLFPSFETFNTKNČIANPNĠNALDESCEDKNRYICKQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.2%; Score 196.5; DB 10; ilarity 32.7%; Pred. No. 5.2e-12; Conservative 25; Mismatches 69;
                                           DB 15;
                                         ; Score 201; DB 15;
; Pred. No. 2.4e-12;
36; Mismatches 81
                                                                                                                          1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/335,009
                                                                                                                                                                                                             45 LLTAVLLSVLLYQWILCQGSNYSTCA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 130, Application US/09919039; Publication No. US20030108871A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/10335009 Publication No. US20040001804A1 GENERAL INFORMATION:
                                         19.6%;
26.0%;
                                                                                  58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                       Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-919-039-130
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  US-10-379-127-25
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TYPE: PRT
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APPLICANT: Goodrich, Ryle
APPLICANT: Goodrich, Ryle
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TAN
TITLE OF INVENTION: OF CELLS THAT EXPRESS DCAL-HY POLYPEPTIDES
TILE REPERENCE: NUVO-01CIP
CURRENT PELLING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR PILING DATE: 2001-03-05
  5;
                                                                   49 SNXDLCASRSADQTVLCQSEWLKYQGKCYWFSNEMKSWSDSYVYCLERKSHLLIHDQLE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 SNYSTCASCPS-----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQE 118
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                                                                                                                                                  SNYSTCASCPS-----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQE
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                                                                                                                                                                                                                                                                                                                                                  Sequence 310, Application US/10125540
Publication No. US20030059875A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFRENCE: PIZALCI
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
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  48; Indels
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Pred. No. 4.6e-14;
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35.0%; Pred. No. *...
Mismatches
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Publication No. US20040005592A1
GENERAL INFORMATION:
APPLICANT: Emtage, Peter C.R.
  22;
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165 SKIFSETCSSVFKWICQ 181
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SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENUTH: 225
TYPE: PRI
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Best Local Similarity
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US-10-125-540-310
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TYPE: PRT
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Search completed: August 10, 2004, 16:32:36 Job time : 41.4761 secs

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Sequence 5.7, Application US/08722126A
Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER ENDABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-0CT-1996
FILING APPLICATION DATA:
PRINCE APPLICATION NUMBER: 11 10955
FILING DATE: 06-APR-1995
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELLEPHONE: (202) 678-5197
TELLEPHONE: (202) 737-3528
INPORMATION FOR SEQ ID NO: 5:
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CARDA CRADE COMPUTED

TELLEPHONE: (202) 737-3528
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TOPOLOGY: linear
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Sequence 22, Appl
                                                                                                                August 10, 2004, 16:13:57 ; Search time 14.7186 Seconds (without alignments) 662.924 Million cell updates/sec
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Sequence 8
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-51-056A-23
US-08-722-126A-6
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PCT-US94-07587-2
US-08-60-095-9
US-08-60-095-9
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US-08-68-342-3
US-09-113-788-3
US-09-352-302-4
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US-08-543-2468-21
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Length 188;

Score 525.5; DB 3; Pred. No. 1.1e-48;

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US-08-543-2468-24
US-08-111-470-10
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61 IGLRNMSGWRWEDGSP
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Best Local Similarity
Matches 75; Conserv
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US-08-722-126A-6
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                                                                                                        CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                           61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFPDNQGVN 120
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                                   1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                        1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                                                                                                                                             LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
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Gaps
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51.4%; Score 525.5; DB 5; Length 1
Best Local Similarity 53.5%; Pred. No. 1.1e-48;
Matches 100; Conservative 29; Mismatches 57; Indels
57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAPA)
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IED PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        RESULT 2
CT-1039-5-04258-5; Sequence 5, Application PC/TUS9504258; GENERAL INFORMATION:
29;
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECTELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248633
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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amino acid
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202-737-3528
100; Conservative
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CITY: Washington
STATE: D.C.
COUNTRY: USA
71P: 20004
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GENERAL INCORPATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
TITLE OF INVENTION: DNA MOLECULES
FILE REFERENCE: DA20 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Version 3.0
SEQ ID NO 33
LENGTH: 76
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121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 PSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCW 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PECHT, Israel
APPLICANT: GUTHWANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SOURNES: 20
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-0CT-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRICH DATE: 06-APR-1995
PRICH DATE: 10-APR-1995
PRICH DATE: 10-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington
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ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/09531056A Patent No. 6455683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08722126A Patent No. 6034227
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Gaps

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us-09-811-367b-1.open.rai

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75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 VEEKDWINSSLEFCLARDSHILVITDNQEMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145
                                                                                                                                                                                                   1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDQAIYAELNLPT-----DSGPESSSPSSLPRDVCQGSPWHQFALKLSCAGIILLVL-
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                                                                                                                                                                                                                                                                                         135 LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
                                                                                                                                                                                                                                                                                                                              Length 114;
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                                                                                                Indels
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APPLICANT: Chang, Chiwen
APPLICANT: Lanier, Lewis L.
APPLICANT: Pallips Jr., Joseph H.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,462
                             36.2%; Score 370.5; DB 5; 58.4%; Pred. No. 2.6e-32; live 18; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 201; DB 2; 26.0%; Pred. No. 1.1e-13; iive 36; Mismatches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: DNAX Research Institute STREET: 901 Callifornia Avenue CITY: Palo Alto STATE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 LLTAVLLSVLLYQWILCQGSNYSTCA--
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08738462
Patent No. 5965401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
Query Match
Best Local Similarity 58.7...
--hes 66; Conservative
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Best Local Similarity 26.05
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415-496-1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: USA
94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-738-462-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLITFPDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
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COMPOTER: FLORDY disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: BROWDY, ROGER IL.
REGISTRATION NUMBER: 25,618
HERDENANTLY NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%; Score 370.5; DB 3 58.4%; Pred. No. 2.6e-32; tive 18; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PECHT=1 PCT
                                                                                                                                                           PECHT=1A
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                                                                            NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PEG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                          FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                                                                                       LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: 114 amino acids
amino acid
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Best Local Similarity 58.49
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: A DI
TITLE OF INVENTION: FUNG
UNDER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein PCT-US95-04258-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-722-126A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSRWMKYGNHCYYFSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Chang, Chiwen
APPLICANT: Aramburu Beltran, Jose
APPLICANT: Aramburu Beltran, Jose
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRAK Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 --SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
COUNDER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.2%; Score 196.5; DB 1; ilarity 32.7%; Pred. No. 2.4e-13; Conservative 25; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECHONE: 415-855-0555
TELEFRAX: 415-845-4166
INFORMATION FOR SEQ 1D NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute
STREET: 901 Callfornia Avenue
STIX: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08650578
Patent No. 5811284
                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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CLONE: 1098617
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hes 53; Conserv
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MOLECULE TYPE: per
IMMEDIATE SOURCE:
                                                                                                                                Palo Alto
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ZIP: 94304
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                                                                                                                                CITY: I
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 HTVNPWNNSLADCSTKESSLLLIRDKDELIHTQNLIRDKAILFWIGLNFSLSEKNWKWIN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SCSCLVAITLG 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                            | Sequence 2, Application PC/TUS9407587
| Sequence 2, Application PC/TUS9407587
| GENERAL INFORMATION:
| APPLICANT: Schering Corp.
| TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND
| TITLE OF INVENTION: RELATED REAGENTS
| NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Schering Corp.
| STREET: One Giralda Farms
| CITY: Meadison
| STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 19.6%; Score 201; DB 5; Length 225; Best Local Similarity 26.0%; Pred. No. 1.1e-13; Matches 58; Conservative 36; Mismatches 81; Indels
                                                   170 GSFLNSNDLEIRGDAKENSCISISQTSVYSEYCSTEIRWICQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 GSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 GSFLNSNDLEIRGDAKENSCISISQTSVYSEYCSTEIRWICQK 212
                       GSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 LLTAVLLSVLLYQWILCQGSNYSTCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07940

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07587
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: DX0397K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08690095
Patent No. 5792648
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 225 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201-822-7039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-07587-2
                                                                                                                                                          PCT-US94-07587-2
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Gaps

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93 EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE
                                                                                                                                                                                                                                                                                                                                                                 Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 --SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
                                                                                                                                                                                                                                                                                                                                                               19.2%; Score 196.5; DB 2; 32.7%; Pred. No. 2.4e-13; tive 25; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
    REGISTRATION NUMBER: 36,749
REPERBENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0095-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
CURTWARE: FASCESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09113788
Patent No. 5969104
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.78
Matches 53; Conservative
                                                                                                                                                    179 amino acids
                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                single
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                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: pepi
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                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304
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                                                                                                                                                                                                                                                                                                                      US-08-688-342-3
                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-113-788-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWYGYRCNCYFISSE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
                                                                                                SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,578
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/175,339
FILING DATE: 29-DEC-1993
ATTONNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET NUMBER: DX0391
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08688342
Fatent No. 5871964
GENERAL INFORMATION:
APPLICANT: AU-Young, Janice
APPLICANT: Gocks, Benjamin G.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDERSS:
ADDRESSEE: ADDRESSE:
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.2%; Score 196.5; DB 2
32.7%; Pred. No. 2.4e-13;
iive 25; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY AGENT INFORMATION:
ZIP: 94304-1104
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 179 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 53; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Por
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-650-578-2
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US-08-688-342-3
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-SCPDRWMKYGNHCYYFSVEEXDWNSSLEFCLARDSHLLVITDNQEM 119
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                                                                                                  20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE 78
                                                                          35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 QAQNDYGPQ---QKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYSTCASCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 RGQKDHGTSIHFEKHHEG----SIQVSIPWAVLIVVLITSLIIALIALIALIAVGKY----NCP
                                         Gaps
                                       15;
   Length 179;
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                                       Indels
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                                                                                                                                                                                                                              150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                               137 --SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10418
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.2%; Score 196.5; DB 5; 27.2%; Pred. No. 2.7e-13;
   DB 3;
ch 19.2%; Score 196.5; DB 3; Similarity 32.7%; Pred. No. 2.4e-13; 53; Conservative 25; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9310418
GENERAL INFORMATION:
APPLICANT: Ziegler, Steven F.
APPLICANT: HjerridA Kathryn A.
TITLE OF INVENTION: Activation Antigen CD69
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REPERENCE/DOCKET NUMBER: 2610-
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 199 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: USA
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Best Local Similarity
Matches 52; Conserv
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PCT-US93-10418-4
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 Query Match
Best Local S:
Matches 53
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                                                                                                                                                                                                                                                 35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                15;
                                                                                                                                                                        19.2%; Score 196.5; DB 2; Length 179; 32.7%; Pred. No. 2.4e-13;
                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09113789
Patent No. 6034219
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
ITLLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              69;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMUNICATION INFORMATION:
TELECHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FRAECSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 179 amino acids TYPE: amino acid
                                                                                                                                                                                                            53; Conservative
 TYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
IMBERARY: GenBank
CLONE: 1098616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: single
linear
                 SS: single
linear
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                                                                                                                                                                                        Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , CLONE: 1098617
US-09-113-789-9
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COUNTRY:
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US-09-113-788-3
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Gaps

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McAulay Fisher Nissen Goldberg & Kiel

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TITLE OF INVENTION: Modified Low-Density Lipoprotein TITLE OF INVENTION: Receptor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                        APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 QEMSILLQVFLSEAF--CWIGL---RNNSGWRWEDGSPIN-----FSRISSNSFVQT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.9%; Score 193; DB 2; Length 270; 30.6%; Pred. No. 9.8e-13; tive 25; Mismatches 53; Indels 25;
                                                                                                    Sequence 4, Application US/09055095
; Sequence 4, Application US/09055095
; Patent No. 2945308
; GENERAL INFORMATION:
APPLICANT: Patterson, Chandra
APPLICANT: Patterson, Chandra
APPLICANT: Sather, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASISED (FOR Windows Version 2.0
SOFTWARE: FASISED (FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,095
FILING DATE: Filed Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0500 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 CAYIQRGTVFAENCILTAFSICQK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 CGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Conservative
Query Match
Best Local Similarity
Matches 44; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: 1902982
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
                                                                            RESULT 14
US-09-055-095-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-055-095-4
                    g
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RESULT 15 US-08-809-494A-2 ; Sequence 2, Application US/08809494A ; Patent No. 5962260

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57 QWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 QEVLKEAANYS-----GPCPQDWLWHEBNCYQFSSGSFNWEKSQENCLSLDAHLLKINST 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 QEMSLLQVFLSEAF--CWIGL---RNNSGWRWEDGSPLN-----FSRISSNSFVQT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
18 9%; Score 193; DB 2; Length 270;
Best Local Similarity 30.6%; Pred. No. 9.88-13;
Matches 44; Constryative 25; Mismatches 53; Indels 2
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,494A
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERERENCE/DOCKET NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
PELEPHONE: 212 986-4090
PELEPHONE: 212 986-9479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 10, 2004, 16:20:31
Job time : 15.7186 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 CGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 CAYIQRGTVFAENCILTAFSICOK 262
                                                                                                                                                                                                                                                                                                                                                                           PRIOR ADTICATION DATA.

APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules B
REGISTRATION NUMBER: 24408
                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSEE: McAulay Fisher N
STREET: 261 Madison Avenue
CITY: New York
                                                                  STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-809-494A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model protein search, OM protein

August 10, 2004, 16:12:27; Search time 11.9788 Seconds (without alignments) 1509.673 Million cell updates/sec on: Run

US-09-811-367B-3 Perfect score:

1029 1 MADSSIYSTLELPEAPQVQD.....GLQASSCEVALQWICKKVLY 188 Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:* Database

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	mast cell function	gene 17.5 protein	natural killer cel	lymphocyte early a	hÑKŘ-Pla protein -	aqkisacutacin beta	natural killer cel	C type lectin, B l	coaqulation factor	rece	natural killer cel	phospholipase-A(2)	NKR-P1 protein hom	HIV gp120-binding	B-cell surface ant	aggretin beta chai	NK-cell receptor P	ρ	natural killer cel	natural killer cel	asialoglycoprotein	scavenger receptor	hepatic lectin 2 -			killer	aggretin alpha cha	asialoglycoprotein	secretory phosphol
SUMMARIES	ID	L LO	150146	A46467	JH0822	I38700	JC7135	PT0374	T28141	JC4691	T42710	PT0372	S48719	B46467	A46274	A43532	JC7105	A35917	C46467	PT0375	I54524	S13165	JC7595	LNRT2	JX0209	WMVZF2	T28140	PC7027	LNHU2A	B56395
	DB		~	N	N	7	N	Ŋ	N	~	C)	N	N	N	7	7	7	7	(1	7	0	7	0	Н	7	Н	7	7	Н	7
	Length	188	257	227	199	225	146	231	156	146	1479	233	1487	223	404	359	146	223	220	216	240	301	742	301	304	167	170	144	311	1326
ð	Query Match	. α	17.7	17.5	16.9	16.0	15.9	15.6	15.1	14.8	14.8	14.7	14.7	•	14.5		14.2	•	14.2	4	14.0	•		ä,	13.5		13.3	13.1	12.9	12.9
	Score	838	182	180.5	173.5	164.5		160.5	155.5	152.5	152.5	151	151	149	149	147.5	146.5	146.5	146	144	144	14	143.5	4	139	'n		3	133	132.5
	Result No.		7	m	4	5	9	7	80	Φ	10	11	12	13	14	15	16	17	₽₹	19	20	21	22	23	24	25	26	27	28	29

secretory phosphol	Kupffer cell recep	hepatic lectin H1	hepatic lectin - c	hepatic lectin - r	proteoglycan core	phospholipase A2 r	phospholipase A2 r	aggrecan precursor	lectin M-ASGP-BP p	T-cell surface gly	Ly-49D-GE antigen	botrocetin alpha c	L-selectin precurs	L-selectin precurs
A56395	A28166	LNHU1	LNCHL	LNRTL	A28452	A53210	A49707	A55182	A42230	A30573	I49049	A47267	809702	A34015
77	1 (1)	Н	Н	Н	N	7	П	Н	N	C)	7	7	Н	П
1465	550	291	207	284	2124	1463	1458	2132	306	262	260	133	323	385
12.9	12.4	12.4	12.3	12.2	12.0	11.9	11.9	11.9	11.8	11.7	11.6	11.6	11.5	11.5
132.5	128	127.5	127	126	123	122.5	122	122	121.5	120.5	119.5	119	118.5	118.5
0-	10	33	34	35	96	37	88	6	0	듸	2	33	14	5

ALIGNMENTS

mast cell function associated antigen - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 05-Nov-1999

C;Accession: I59421

Figurhmann, M.D.; Tal, M.; Pecht, I.

Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1895

A,Title: A secretion inhibitory signal transduction molecule on mast cells is another C A,Reference number: IS9421

A,Reference number: IS9421

A,Status: preliminary; translated from GB/EMBL/DDBJ

A,Molecule type: mRNA

A,Residues: 1-188 <RES>
A,Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C,Genetics:

A;Gene: mafa

ó Gaps 0; Length 188; Indels 21; Query Match 81.4%; Score 838; DB 2; Best Local Similarity 80.7%; Pred. No. 1.3e-74; Matches 151; Conservative 15; Mismatches 21;

09 1 MADNSIYSTIELPAAPRVQDDSRWKVKAVLHRPCVSYLVWVALGLITVIIMSLLLYQRTL 60 1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL g à

61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120 à

61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLIFFPDNQGVN 120 g

121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180 à

181 WICKKVL 187 121 임 ₽

|||:||| WICEKVL 187 181 g

RESULT I50146

gene 17.5 protein - chicken

C'Species Gallus (chicken)
C'Species Gallus (chicken)
C'Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C'Accession: I50146
R'Bernot, A.; Zoorob, R.; Auffray, C.
R'Bernot, A.; Zoorob, R.; Auffray, C.
R'Jitle: Linkage of a new member of the lectin supergene family to the chicken Mhc gene; A.Reference number: I50146; MUID:94164691; PMID:8119728
A.Accession: I50146

A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA

```
lymphocyte early activation antigen AIM/CD69 - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 08-Oct-1999
C;Accession: JH0822; I56167; S60753
R;Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M. Exp. Med. 178, 537-547, 1993
A;Title: Modecular cloning, expression, and chromosomal localization of the human earlimiting receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-199 <RES>
A; Residues: 1-199 <RES>
A; Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1; PID:g291898
A; Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1; PID:g291898
By: A:G: Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
Bur. J. Immunol. 24, 1692-1697, 1994
A; Title: Structure of the gene coding for the human early lymphocyte activation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: EMBL:Z30426; NID:g525242; PIDN:CAA83017.1; PID:g558352
C,Comment: This protein is the earliest inducible cell surface glycoprotein expressed i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C) #status predicte
#status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Title: Expression cloning of the early activation antigen CD69, a type II integral A,Reference number: I56167; MUID:93267093; PMID:8496594
                                           119 LVDCDGKGATLMLIQDQEELRFILDSIKEKYNSFWIGLRYTLPDMNWKWINGSTLNSDVL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 ALIALSVGOYNCPGOYTFSMPSDSHVSSCSEDWVGYORKCYFISTVKRSWTSAQNACSEH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGGPALSLRI-LTNSLIQRCG 163
      100 LKFCADKGSHLLTFPDNQGVKLFGEYLGQDF--YWIGLRNI---DGWRWEGGPALS---L 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FAMVALGLITVILM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 NSSLH-----PESGQENDAT-----SPHFSTRHEGSFQVPVLCAVMNVVFITILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:9397939
as GLu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-199 <LOP>
A;Cross-references: GB:Z22576; NID:g397938; PIDN:CAA80298.1;
A;Note: the authors translated the codon CAA for residue 110
B;Hamann, J.; Piebig, H.; Strauss, M.
J. Immunol. 150, 4920-4927, 1993
                                                                                                                                                                         A; Reference number: S60753; MUID: 94298875; PMID: 8026529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: JH0822; MUID: 93340630; PMID: 8340758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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llarity 23.8%; Pred. No. 1.5e-09;
Conservative 36; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: GDB:CD69
A;Cross-references: GDB:132925; OMIM:107273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: I56167
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Map position: 12p13-12p12
C,Superfamily: C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: S60753
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-199 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JH0822
                                                                                                                                 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              natural killer cell receptor P1 - mouse
N.Alternate names: NKR-P1 protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A46467; A46502; Ā46456
R;Giorda, R; Trucco, M.
J. Immunol. 147, 1701-1708, 1991
A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Reference number: A46467; MUID:91349596; PMID:1880421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-109,'H',111-181,'D',183-227 <G12>
A;Cross-references: GB:X64716; NID:953395; PIDN:CAA45971.1; PID:9817989
A;Cross-references: GB:X64716; NID:953395; PIDN:CAA45971.1; PID:9817989
A;Cross-references: GB:X64716; NID:953395; PIDN:CAA45971.1; PID:9817989
A;Cross-reference Extracted from NCBI brobback Cell link
B;Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
A;Title: CDNA cloning of mouse NRA-P1 and genetic linkage with LY-49. Identification of A;Reference number: A46456; MUID:92013158; PMID:1680927
A;Accession: A46456
A;Molecule type: mRNA
A;Cross-references: GB:M77753; NID:9198569; PIDN:AAA39366.1; PID:9198570
A;Cross-reference extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)
C;Superfamily: natural killer cell receptor Pi; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>
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A; Residues: "MHLLCT", 1-27 <GIO>
A; Residues: "MHLLCT", 1-27 <GIO>
A; Residues: "MHLLCT", 1-27 <GIO>
A; Cross-references: GB:MM7676; NID; 9200058
A; Experimental source: A-LAK cells, C57BL
A; Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence st Giorda w. R.; Weisbergy, E.P.; Ip, T.K.; Trucco, M.
J. Immunol. 149, 1957-1963, 1992
A; Title: Genomic structure and strain-specific expression of the natural killer cell replacesion: A46502
A; Status: preliminary
A; Status: preliminary
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                                                                                                                                                                                                                                                                                             61 LV--RVLIQKPSIEKCYVLIQENINKTTDCSAKLECPQDWLSHRDKCFHVSQVSNTWEEG 118
                                                                                                                                                                                                                                                                                                                                                                                      88 YFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG---WRWE 144
                                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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                                                                                                                                                                                                                                                        32 RPHLSRFAMVALG----LLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCY
                                                                                                                                                                                                Gaps
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A;Cross-references: GB:M88072; NID:g505324; PIDN:AAA48558.1; PID:g505325 C;Superfamily: C-type lectin homology
F;129-241/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 DGSA----FTWRPVFELRGGGRCAYLNGDGISSALCHSEKFWVCSR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPALSLRILINSLI-----ORCGAIHRNGLQASSCEVALOWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MADSSIYSTLELPEAPQVQDESRWKL---KAVLHRPHLSRFAMVALGLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                            72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%; Score 180.5; DB 2; 26.7%; Pred. No. 3.5e-10; ive 33; Mismatches 95;
                                                                                                                             Score 182; DB 2;
Pred. No. 2.9e-10;
                                                                                                          17.7%; sc. No. 28.7%; Pred. No. 28. 7%; Mismatches
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Best Local Similarity 26.7%
Matches 58; Conservative
                                                                                                                                                                                                48; Conservative
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary A; Molecule type: DNA
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C;Accession: PT0374
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
A;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
A;Hitle: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I:
A;Reference number: PT0372; MUID:91178434; PMID:2007850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
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A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A;Experimental source: clone cB12
                                                                                                                  95 DWNSSLKFCAD--KGSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI-DG--WRWEG 145
                                                                                                                                                    45 TWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKWSD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;71-96/Domain: transmembrane #status predicted <TRA>
F;27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLSGTAADCPS---EWSSYEGHCYKPFDEPK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctype lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPEKLTAEVLGIICIVLMATVLKTIVLIPFLEQNNSSPNTRTQKARHCGHCPEEWITYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 SHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL-RNIDGWR
35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 PHLSRFAMVALGLLTVILMSLLMYQRIL-----CCGSKDSTCSHCPSCPILWTRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: PT0374
A, Molecule type: mRNA
A, Residues: 1-231 - GHOU.>
A, Cross-references: EMBL:X54869; NID:g35060; PIDN:CAA38651.1; PID:g35061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-type lectin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                               splice form 1 - human
                                                                                                                                                                                                                                     146 GPALSLRILINSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                             GTKLDYKDWREQFECLVSRIVNNEWLSMDCGTTCSFVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 160.5; DB 2 24.4%; Pred. No. 3.3e-08; tive 29; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GDB:9787095
A,Map position: 12p13-12p13
C,Superfamily: natural killer cell receptor P1; C,Superfamily: natural killer cell receptor P1; C,Keywords: glycoprotein; transmembrane protein P;71-96/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: natural killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                            natural killer cell receptor group 2-C,
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                                              1 MGRFIFVSFGLLVVFL
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A;Gene: GDB:KLRC2; NKG2-C
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Les 41; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ocision beta chain precursor - sharp-nosed viper
NyAlternate names: fibrinogenlytic venom protein
CySpecies: Agkistrodon acutus Gsharp-nosed viper)
CyBecies: Adxistrodon acutus Gsharp-nosed viper)
CyAccession: JC7135; Pc7038
RyCheng, X.; Olan, Y.; Liu, Q.; Li, B.X.Y; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A/Title: Purification, characterization, and cDNA cloning of a new fibrinogenlyt
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Residues: J-146 cCHE>
A;Residues: J-146 cCHE>
A;Residues: J-146 cCHE>
A;Resperimental source: venom gland
A;Accession: PC7038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSLKFCADKGSHLLTFPDNQGVKLFGEYLGQD---FYWIGLR---NIDGWRWEGGPALS- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                 Cispecies: Homo sagiens (man)
Cispecies: Homo sagiens (man)
Cispecies: Homo sagiens (man)
Cispecies: 123-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
Ciscossion: 138700
Cispecies: Cispecies: 138700; Cispecies: 138700; MUID:94358407; PMID:8077657
A; Fitle: Human NKR-PlA: A disulfide-linked homodimer of the C-type lectin surfixed streamence number: 138700; MUID:94358407; PMID:8077657
A; Accession: I38700
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: manna, Ashabilitation (manna, Ashabileos: 1-225 cress)
A; Residues: 1-225 cress
A; Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PID:9544496
C; Superfamily: natural killer cell receptor Pl; C-type lectin homology
F; 94-210/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDQQAİYAEİNLPTDSGPESSSPSSLPRDVCQGSPWHQFAL----KLSCAGIILLVLVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LTVILMSLLMYQRILCCG----SXDSTCSH--CPSCPILWTRNGSHCYYFSMEKKDWN
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C;Keywords: disulfide bond; heterodimer; venom
E;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LRILINSLIQRCGAIHRNGLQASSCEVALQWICKKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 16.0%; Score 164.5; DB 2;
Local Similarity 27.4%; Pred. No. 1.3e-08;
Les 60; Conservative 32; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 24-50,59-83;102-107;112-114 < CH2>
                        164 AIHRNGLQASSCEVALQWICKK 185
                                                                 175 FLKNTEVSSMECEKNLYWICNK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MADSSIYSTLELP--EAPQ--
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Matches 48; Conservative
                                                                                                                                                                                                                                  hNKR-Pla protein - human
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Best Local S:
Matches 60
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C;Species: Mus musculus (house mouse)
C;Date: 11.-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
C;Date: 11.-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
C;Accession: T42710
B;Wu, K.; Yuan, J.; Lasky, L.A.
J Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the macrophage mannose receptor type C 1
A;Accession: T42710
A;Accession: T42710
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PT0372
Nalternate names: NKG2-A; NKG2-B
N;Alternate names: NKG2-A; NKG2-B
N;Alternate names: NKG2-A; NKG2-B
C;Gordians: natural killer cell receptor group 2, splice form B
C;Gordians: natural killer cell receptor group 2, splice form B
C;Gordians: natural killer cell receptor group 2, splice form B
C;Gordians: natural killer cell receptor group 2, splice form B
C;Gordians: natural killer cell receptor group 2, splice form B
C;Gordians: natural killer cell receptor group 2, splice form B
C;Gordians: J-31, ABO-173, INT0-1003, 1931
A;Accession: PT0372; PT0372; MUD191178434; PMID:2007850
A;Reference number: PT0372; MUD191178434; PMID:2007850
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                                                                                                                                                                 N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 DSTCSHCPSCPILWTRNGS--HCY-YFS----MEKKDWNSSLKFCADKGSHLLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        659 DPTPSLTGSCPQGWVSDPKLRHCYKVFSSERLQEKKSWIQALGVCRELGAQLLSLASYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --FPDNOGVKLFG----BYLGODFYWIGLRNID-----GWRWEGGPALSLRILTNSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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Pred. No. 2.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 152.5; DB 2
32.0%; Pred. No. 1.4e-06;
ive 12; Mismatches 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --IQRCGAIHRNGLQ--ASSCEVALQWICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDIRGCAVLDLASLÓWVPMQCQTQLDWICK
                                                                                                                                           mouse
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23.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Conservative
                                                                                                                                           macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                   mannose receptor,
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A, Residues: 1-146 < MATI->
A, Residues: 1-146 < MATI->
A, Residues: 1-146 < MATI->
A, Cross-references: DDBJ-198332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
A; Cross-references: DDBJ-198332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
A; Experimental source: venom
R; Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A; Title: The primary structure of coagulation factor IX/factor X-binding protein isolate otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A; Reference number: A39332; MUID:91332000; PMID:1831197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trimeresurus flav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation factor IX/factor X-binding protein chain A precursor - habu C;Species: Trimeresurus flavoviridis (habu) C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000 C;Accession: JC46611, B39332; JC4330 R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T. Biochem. Biophys. Res. Commun. 220, 382-387, 1996 A;Title: cDNA cloning of IX/A-BP, a heterogeneous two-chain anticoagulant protein from A;Reference number: JC4690; MUID:96184662; PMID:8645314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Molecule type: protein
A, Residues: 24-146 <ATO>
A, Actoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
G, Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
G, Aritle: Blood coagulation factor IX-binding protein from the venom of Trimeresurus
A, Reference number: GC4329; MUID:96318509; PMID:8749314
A, Accession: JC4330
A, Molecule type: protein
A, Residues: 24-146 <ATO:
C, Superfamily: terranectin; C-type lectin homology
C, Superfamily: terranectin; C-type lectin homology
C, Superfamily: terranectin; C-type lectin homology
C, Superfamily: factor IXX binding protein chain B #status predicted <AMT>
F;24-146/Product: factor IXX binding protein chain B #status predicted
E;25-142/Domain: C-type lectin homology <ALCH>
E;25-142/Domain: G-type lectin homology <ALCH>
E;25-36,53-142,119-134/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNSSIKRCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG----WRWEGGPALS- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WTSSQNNCSALGASLAVFDSAEDLSFTMRHKGSSPHWVGLSR-EGKEHPWEWVNRSPLSH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DWNSSLKFCADK--GSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145
                                                                                                                                                                                                                                                                                                         95
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                                                                                                                                                                                                                                                                                                    AMVALGLLTVILMSLLMYQRILCCGSKDSTCSH----CPSCPILWTRNGSHCYYFSMEKKD
                                                                                                                                                                                                                                                                                                                                                                                   ----PHPOPCAOCPFDWIGFRGKCYYFSEDESN
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                                                                                                                                   Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 155.5; DB 2;
Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 -LRILITUSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 LFQVQGDGL---CAYLGDAĞLSSSHCSTRRNWVCTK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70;
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24.5%; Pred. No. 1.2e-07;
iive 25; Mismatches 70
                                                                                                                                                                                                             24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               3 AVFTVLLITAVAFAVQAFQ--
                                                                                                                              15.1%;
                                                                                                                                                                      25.0%;
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Best Local Similarity 24.5
Matches 39; Conservative
                                                                                                                                                                                                                      Conservative
16
1; 74/3; 110/2
                                                                                                                 Query Match
Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B39332
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A; Map position: 1
A; Introns: 17/1;
                                                                                                                                                                                                                                                                                                    39
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Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A, Title: Sequence and expression of a membrane-associated C-type lectin that exhibits C
A, Reference number: A46274; MUID:92390446; PMID:1518869
                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                   -YQRILCCGSKDST----CSHCPSCPILWTRNGSHCYYFSMEKKDWNSSL 100
                                                                                                                                                                                                                                                                                                                                                                                                             60 CVLVLSVQKSSVQKICADVQENRTHTTDCSVNLECPQDWLSHRDKCFRVFQVSNTWEEGQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 KFCADKGSHLLTFPDNQGVKLFGEYLGQDF--YWIGLRNI---DGWRWEGGPALS---LR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 ELPEKSKOOBIYOELTRLKA-----AVGELPEKSKOOBIYOEL--TOLKAAV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 SNRFTWMGLSDINQECTWQWYDGSPLIPSFKQYWNRGEPNNVGEEDCAEFSGNGWNDDKC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTF--PDNQGVKLFGEYL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 GODFYWIGLRNID---GWRW-EGGPALSL-----RILINSLIQR-CGAIHRNGLQASSC 175
                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV gp120-binding C-type lectin - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- RWKLKAVLHRPHLSRFAMVALGLLTVILMSL
                                                                                                                                                                                                                                                                  11 ELPEAPQVQD--ESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 ERLCHPCPWEWTFFQGNCYFMSNSQRNWHDSITACKEVGAQLVVIKSAEEQNFLQLQSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: placenta
A,Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)
C; Superfamily: C-type lectin homology
F; 256-377/Domain: C-type lectin homology <LCH>
                                                                                                                                                                    40;
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                                                                                                 Length 223;
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                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILTNSLIQRCGALHRNGLQASSCEVALQWICKKVL 187
                                                                                                 ; DB 2;
4.2e-07;
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14.5%; Score 149; DB 2;
Best Local Similarity 25.8%; Pred. No. 7.9e-07;
Matches 49; Conservative 29; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :: | :| |: | ITGDTENGSCASISGDKVTSESCSTDNRWICQKEL
                                                                                                                                                           36; Mismatches
                                      C-type lectin homology <LCH>
                                                                                                 14.5%; Score 149; 22.8%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Accession: A46274
R;Curtis, B.M.; Scharnowske, S.; Watson, A.J.
      C; Keywords: transmembrane protein F; 94-210/Domain: C-type lectin hom
                                                                                                                                                                                                                        6 IYSTLELPEAPQVQDES-
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: nucleic acid
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                                                                                                                          Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                             54 LM-----
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                                                                                                    Query Match
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() Species: Mus musculus (house mouse)

() Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999

() Accession: B46467

R; Giorda, R.; Trucco, M.

J. Immunol. 147, 1701-1708, 1991

A; Richera A family of genes selectively coexpressed in adherent lymphokine-activated kill A; Reference number: A46467; MUID:91349596; PMID:1880421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D30779; NID:g1375042; PIDN:BAA06443.1; PID:g691754
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II
F;181.222/Domain: fibronectin type II repeat homology <2F1>
F;380-503/Domain: C-type lectin homology &LCH>
      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                     56 YQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPD 115
                                                                                                                                                                                                                               116 NQGVKLFGEYLGQDFYWIGL-RNIDGWRW--EGGPALSLRILTNSLIQ-RCGAIHRNGLQ 171
                                                                                                                                                                                                                                                                                                                                                                       160 BEEMKFLS--IISPSSWIGVFRNSSHHPWVTMNGLAFKHEIKDSDNAELNCAVLQVNRLK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CPILWTRNGSH--CYYFS-MEKKDWNSSLK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHILIWCATTSRYEEDEKWGFCPDPTSMKVFCDATWQRNGSSRICYQFNLLSSLSWNQAHS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 SCLMQGGALLSIADEDEEDFIRKHLSKVVKEVWIGLNQLDEKAGWQWSDGTPLSYLNWSQ 321
                                                                                                                          -KLIVGILGIICLILMASVVTIVVIPSTLIQ 99
                                                                   ---SLLM 55
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 FCADKGSHLLTFPDNQGVKLFGEYLGQ--DFYWIGLRNID---GWRWEGGPALSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-223 cGIO>
A;Cross-references: GB:N7677; NID:g200060; PIDN:AAA39823.1; PID:g200061
A;Cross-references: NK cells, C57BL7B
A;Bore: sequence extracted from NCBI backbone (NCBIN:52380, NCBIP:52381)
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
      36;
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      86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67; Indels
                                                             7 YSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EITPGPFVEHHCGTLEVVSAAWRSRDCESTLPYICKRDL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RILTNSLIQ-RCGAIH -- RNGLQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.7%; Score 151; DB 2; 27.0%; Pred. No. 2e-06; iive 21; Mismatches 6
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRILCCGS----KDSTCSHCPS---
   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAQCGSSIIYHCKHKL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                    ASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
   Conservative
                                                                                                                          YHCKDLPSAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1487 <HIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
   45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218
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A;Title: Identification of a human protein homologous to the mouse Lyb-2 B cell different A;Reference number: A43532; MUID:90278102; PMID:2141045
A;Recession: A43532; MUID:90278102; PMID:2141045
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-359 <VON>
A;Cross_references: GB:MS4992; NID:g187262; PIDN:AAA36189.1; PID:g187263
C;Genetics: GB:Mp-9p
A;Gene: GDB:CD72
A;Gene: GDB:CD72
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Best Local Similarity 27.3%; Pred. No. 9.7e-07;
Matches 38; Conservative 19; Mismatches 61; Indels 21.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

(without alignments) 1337.256 Million cell updates/sec August 10, 2004, 16:05:41; Search time 7.32035 Seconds ü Run

US-09-811-367B-3 1029

1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 Perfect score: Sequence:

BLOSUM62 Scoring table:

141681 segs, 52070155 residues Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q9mzk9 macaca mula P27811 mus macaca mula P27811 mus macaculu Q9mz41 pan troglod Q07108 homo sapien Q9mz41 pan troglod P28717 mus musculu Q9gme8 pan troglod P28717 homo sapien Q9mz51 mus musculu P26715 homo sapien Q9mz71 mus musculu Q9mz71 mus musculu Q9mz71 tattus norv P27814 mus musculu Q9y184 homo sapien Q9y184 homo sapien P26718 homo sapien Q97878 macaca mula Q9mzk6 macaca mula Q9mzk6 macaca mula Q9mzk6 macaca mula Q9mzk6 macaca mula Q9mzk6 macaca mula Q9mzk6 macaca mula Q9mzk6 macaca mula Q9mzk6 macaca mula Q9mzk9 agkistrodon P49300 mus musculu P14370 fowlpox vir Q9smz49 macaca mula Q9mz53 macaca mula Q9mz53 macaca mula Q9mz73 macaca mula Q9mz73 macaca mula Q9mz73 macaca mula P07307 homo sapien P07307 homo sapien P07307 mus musculu
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P10716 rattus norv	P07306 homo sapien	FOZ/OJ GALLUS GALL	F3492/ Mus musculu	P02706 rattus norv	P81397 agkistrodon	P81509 crotalus ho	P81114 trimeresuru	P07897 rattus norv	P49259 bos taurus	P49260 oryctolagus	Q61282 mus musculu
KUCR_RAT	LECH HUMAN	THOM CHICK	LECH MOOSE	LECH_RAT	RHCA_AGKRH	CHBB_CROHO	ABA4_TRIAB	PGCA RAT	PA2R_BOVIN	PA2R RABIT	PGCA_MOUSE
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21158386; PubMed=11261935;
Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rheaus monkey decidua.";
Immunogenetics 53:69-73(2001).
--- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
--- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                 ΰ
      CD94 MACMU STANDARD; PRT; 179 AA.
Q9MZK3; O9GK91; Q9MZK8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Natural killer cells antigen CD94 (NK cell receptor)
lectin-like receptor subfamily D, member 1).
MACMED OF CD94.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDILINE=2032487; PubMed=10866118;
LaBonte M.L., Levy D.B., Letvin N.L.;
"Characterization of Fresus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B,
                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenetics 51:496-499(2000).
                                                                                                                                                              Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF190931; AAF74527.1; -. EMBL; AF190932; AAF74528.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                Cercopithecinae; Macaca.
                                                                                                                                                                                                                               NCBI TaxID=9544;
RESULT 1
CD94_MACMU
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us-09-811-367b-3.open.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 LKFCADKGSHLLTFPDNQGVKLFGEYLGQDF--YWIGLRNI---DGWRWEGGPALS---L 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MADSSIYSTLELPEAPQVQDESRWKL---KAVLHRPHLSRFAMVALGLL----TVILMSL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 IMYORILC-----CG----SKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; P800615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; P850041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
DOMAIN
1 CYTOPLASMIC (POTENTIAL).
TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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CD3241; 043321; 043773; Q9UBE3; Q9UEQ0;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-211 as antigen CD94 (NK cell receptor)
16-Ctin-like receptor subfamily D, member 1) (KP43).
KLRDI OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.5%; Score 180.5; DB 1; Length 227; 26.7%; Pred. No. 7.8e-11;
                   FUNCTION: May function as signal-transmitting receptor. SUBUNIT: Homodimer; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                      -:- SUBCELLULAR LOCATION: Type II membrane protein.
-:- TISSUE SPECIFICITY: Natural killer cells.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> L (IN REF. 2).
0599A2587DF0B615 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
Pram; PR00059; Lectin_C. 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
J. Immunol. 147:3229-3236(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 S
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HSSP; P22897; 1EGG.
MGD; MGI:107540; Klrbla.
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186
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93 2
94 1
122 2
189 2
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227 AA;
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                                     HSSP; P22897; IEGG.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; Lectin_c: 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS00611; C_TYPE_LECTIN_2; 1.
Antiqen; Receptor; Glycoptotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                     MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
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                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
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MEDLIAGA R., Trucco M.;

"Mouse NKR-Pl. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells.";

J. Immunol. 147:1701-1708(1991).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                       EXTRACELLUIAR (POTENTIAL).
C-TYPE LECTIVI (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 LWENGSALSOYLFPSFETFKPKNCIAYNSKGNALDESCETKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2) (NKR-P1.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 180.5; DB 1; Length 179;
Pred. No. 6e-11;
7; Mismatches 68; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of a natural killer cell gene complex on mouse chromosome 6.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Natural Killer cell surface protein Pl-2 (NKR-Pl
KLRBIA OR LY55A OR LY55.
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/FTId=VSP_003055.
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/FTId=VSP 003
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AF190933; AAF74529.1; -. AF294886; AAG34498.1; -.
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31.8%;
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83
132
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98
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P27811;
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TRANSMEM
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From Manner C. Schwerz M. S. Septensch S. Schwerz M. Schass H. Schnerch S. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz M. Schwerz 
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                                                                                                                      MEDLINE-96011848; PubMed=7589107;
Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
Lanier L.L.;
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                       Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A., Lehrach H., Francis F., Lopez-Botet M.;
"Structure of the human CD94 C-Type lectin gene.";
                                                                                                                                                                                    "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tohma S., Inoue T., Yamamoto K., Juji T.; A alternatively spliced form of the human CD94 gene."; Immunogenetics 48:87-88(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Biassoni R.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=3; Synonyms=CD94 alt;
IsoId=Q11241-3; Sequence=VSP 003052;
ISOUE SPECIFICITY: Natural kilter cells.
SIMILARITY: Contains: 1 C-type lectin family domain.
DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type II membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
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Name=2; Synonyms=CD94-B;
IsoId=Q13241-2; Sequence=VSP_003053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=98267245; PubMed=9601951;
                                                                                                                                                                                                                                                                                                       MEDLINE=98139529; PubMed=9472066;
                                                                                                                                                                                                                                                                                                                                                                                  Immunogenetics 47:305-309(1998).
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                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
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(Human)
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                     NCBI_TaxID=9606;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. . .) (FOTENTIAL).
N'LINKED (GLCNAC. . .) (FOTENTIAL).
MAVFKTTLWRINGSGTIGHICLSLMATIGHILKNS. -> MAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0005960; P:antimicrobial humoral response (sensu Inver. .; TAM.
GO; GO:0007166; P:call surface receptor linked signal transdu. .; TAM.
InterPro; IPR001304; Lectin_C.
Ffam; PR00159; lectin_c, I.
SMART; SM00034; CLECT; I.
SMART; SM00034; CLECT; I.
ANGELIFE; PS0615; CTYPE_LECTIN_1; FALSE_NEG.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GTLGIİCLSİMATLGİLLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWYGYRC
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SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last amocation update)
Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 IWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.3%; Score 178.5; DB 1; Length 179; 31.8%; Pred. No. 9.5e-11; ive 17; Mismatches 68; Indels 31.
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L -> LQ (In isoform 2).
/FTIG=VSP 003053.
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                                                                                                                                                                                EMBL; U30610; AAC50291.1; -.
EMBL; Y14287; CAA74663.1; -.
EMBL; Y14288; CAA74663.1; JOINED.
EMBL; AJ000673; CAA042230.1; -.
EMBL; AJ00001; CAA0345.1; -.
EMBL; AB010084; BAA24460.1; -.
EMBL; BC028009; AAH28009.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 AA; 20497 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                              HGNC:6378; KLRD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
72
174
166
83
132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105
                                                                                                                                                                                                                                                                                                                                                                        PDB; 186E; 15-JUN-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
98
61
89
152
132
132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD94 PANTR
Q9MZ41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
CD94 PANTR
ID CD94 PX
AC Q9MZ41,
DT 28-FEB-
DT 10-OCT-
DE NATURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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TISSUE=Blood;
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                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptors.
                                                               85
                                                                                                                                                                                                                          HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
SMOSTIE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSTIE; PS50041; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                      MEDLINE=21623889; PubMed=11751968; Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhberg M., Parham P.; Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 168:240-252(2002).
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                            Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                    MEDLINE=20350666; Pubmed=10894168; Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L., Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L., Parham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL)

N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.3%; Score 178.5; DB 1; Length 179; 31.8%; Pred. No. 9.5e-11; ive 17; Mismatches 68; Indels 31
                                                                                                                                                                                         evolution of NK cell receptor systems demonstrated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2; Synonyms=CD94-B;
Isola=Q9MZ41-2; Sequence=VSP 003056;
-!- TISSUE SPECIFICITY: Netural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7244D99E8D9587E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L -> LQ (in isoform 2).
/FIId=VSP_003056.
                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comment=Additional isoforms seem to exist;
D, member 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1; Synonyms=CD94-A;
IsoId=Q9MZ41-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                      comparison of chimpanzees and humans.";
Immunity 12:687-698(2000).
lectin-like receptor subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF259054; AAF86964.1; -.
                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20493 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
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83
132
105
                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 54; Conserv
                                                                              NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
98
61
83
152
83
132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P22897;
                                                                                                                                                                                                                                                                                                                                       NKG2 genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                           "Rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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7;

Gaps

31;

54; Conservative

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HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                              14 GTLGIICLSLMATLGIILKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC 70
-KDSTCSHCPSCPILWTRNGS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F., "Structure of the gene coding for the human early lymphocyte activation antigen CD69: a C-type lectin receptor evolutionarily related with the gene families of natural killer cell-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R., Esch F., Sanchez-Madrid F.;
"Molecular cloning, expression, and chromosomal localization of the human earliest lymphocyte activation antigen AIM/CD69, a new member of the C-type animal lectin superfamily of signal-transmitting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of the early activation antigen CD69: a type II membrane glycoprotein related to a family of natural killer cell activation antigens.";

Eur. J. Immunol. 23:1648-1648 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 31, Last annotation update)
16-MAR-2010 antigen CD69 (Barly T-cell activation antigen p60)
(GP32/28) (Leu-23) (MLR-3) (EA1) (BL-AC/P26) (Activation inducer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamann J., Fiebig H., Strauss M.; "Expression cloning of the early activation antigen CD69, a type II integral membrane protein with a C-type lectin domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=93314711; PubMed=8100776;
Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 96-103; 128-146 AND 189-199.
                                                                                                                                                                                                                                                                                                                                           129 LWENGSALSQYLFPSFETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                142 RWEGGPALSLRILTNSLI---QRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta; MEDLINE=94298875; PubMed=8026529; MEDLINE=94298875; PubMed=8026529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93267093; PubMed=8496594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Blood;
MEDLINE=93340630; PubMed=8340758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunol. 150:4920-4927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exp. Med. 178:537-547(1993).
GLLTVILMSLLMYQRILCCGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule) (AIM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alderson M.R.;
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                        cells, and platelets.
SUBUNIT: Homodimer; disulfide-linked.
SUBCELLUIAR LOCATION: Type II membrane protein.
IISSUE SPECIFICITY: Expressed on the surface of activated T-cells, B-cells, natural killer cells, neutrophils, eosinophils, epidermal Langerhans cells and platelets.
DEVELOPMENTAL STAGE: Earliest inducible cell surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903(2002).
-!- FUNCTION: Involved in lymphocyte proliferation and functions as signal transmitting receptor in lymphocytes, natural killer (NK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acquired during lymphoid activation.

INDUCTION: By antigens, mitogens or activators of PKC on the surface of T and B Lymphocytes. By interaction of IL-2 with the PJ5 IL-2R on the surface of NK cells.

PTM: CONSTITUTIVE SER/ITHR PHOSPHORYLAPION IN BOTH MATURE THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR001304, Lectin C.
Pfam; PF00059; lectin c; 1.
SMART; SM00014, CLECT; 1.
PROSITE; PS00615; CTYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; CTYPE_LECTIN 2; 1.
Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 C-type lectin family domain. DATABASE: NAME=PROW; NOTE=CD guide CD69 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd69.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0004888; F:transmembrane receptor activity; TAS
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BY SIMILARITY.
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EMBL, 222576; CAA80298.1; -.
EMBL, 230426; CAA83017.1; -.
EMBL, 230430; CAA83017.1; JOINED.
EMBL, 230427; CAA83017.1; JOINED.
EMBL, 230429; CAA83017.1; JOINED.
EMBL, 230428; CAA83017.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; BC007037; AAH07037.1; -. JH0822; JH0822.
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PDB; 1E81; 18-JUL-03.
Genew; HGNC:1694; CD69.
MIM; 107273; -.
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PIR; J
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                                                                                                                                                                                                                                                                52 SL--LMYQRILCCGSKDSTC---SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADK 106
                                                                                                                                                                                                                                                                                                       57 ALIALSVGQYNCPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEH 116
                                                                                                                                                                                                                                                                                                                                                                               117 GATLAVIDSEKDMNFLKRYAGREEHWVGLKKEPGHPWKWSNGKEFNNWFNVTGS--DKCV 174
                                                                                                                                                                                                                                                                                                                                                 107 GSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGGPALSLRI-LTNSLIQRCG 163
                                                                                                                                                                                                           ---FAMVALGLLTVILM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of the early activation antigen CD69: a type II membrane glycoprotein related to a family of natural killer cell activation antigens.";

Bur. J. Immunol. 23:1643-1648(1993).

-!- FUNCTION: Involved in lymphocyte proliferation and functions as a signal transmitting receptor in lymphocytes, natural killer (NK) cells, and platelets.

-!- SUBUNIT: Homodimer; disulfide-linked.

-!- SUBUNIT: Homodimer; disulfide-linked.

-!- SUBCELDULAR LOCATION: Type II membrane protein.

-!- TISSUE SPECIPICITY: EXPRESSED ON THE SUBFACE OF ACTIVATED T CELLS, B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS AND PLATELETS.

-!- DOWNINDL STARGE: Barliest inducible cell surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-9314711; PubMed=8100776;
Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

1722269902F880FB CRC64;
                                                                                                                                              35;
                                                                                                     Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acquired during lymphoid activation.
-!- INDUCTION: By the activation of T lymphocytes.
-!- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE THYMOCYTES AND ACTIVATED T LYMPHOCYTES (BY SIMILARITY).
                                                                                                                                              Indels
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                                                                                                     DB 1;
                                                                                                                                                                                3 DSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSR----
                                                                                                     16.9%; Score 173.5; DB 1
23.8%; Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 AA.
                                                                                                                                            36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 FLKNTEVSSMECEKNLYWICNK 196
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                                                             22559 MW;
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199 AA;
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Best Local Similarity
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  DISULFID
                                                           SEQUENCE
                                          CARBOHYD
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InterPro; IRPO01304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SWART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                 Glycoprotein.
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                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
C-TYPE LECTIN.
BY SINILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANTS ASP-60 AND 232-TYR-ARG-233 DEL. MEDLINE=20350666; PubMed=10894168; Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L., Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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Q9GMEB; Q9MZ38; Q9MZ40;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
NKG2-C type II integral membrane protein (NKG2-C activating)
                                                                                                                                                       Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 168; DB 1;
Pred. No. 1.2e-09;
                                Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFEZEII.
SMART; SM0034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Mismatches
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                        InterPro; IPR001304; Lectin_C.
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      removed. Usage by and for commercial sht (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 SHCYYFSMEKKDWNSSLKFCADKGSHLLIFFDNQGVKLFGEYLGQDFYWIGL-RNIDGWR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCS-----HCPSCPILWTRNG 83
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MEDLINE=98350122; PubMed=9683661;
Glienke J., Sobarov Y., Brostjan C., Steffens C., Nguyen C.,
Lehrach H., Hofer E., Francis F.;
"The genomic organization of NKG2C, E, F, and D receptor genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-D (in allele NKG2-C*I01).

Missing (in allele NKG2-C*I01).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                             SMART; SM0034; CLECT; 1.
SMOSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 WE--GGPALSLRILINSLIQ-RCGAIHRNGLQASSCEVALQWICKKVLY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 WVIINGLAFKHEIIDSDHAELNCAVLQVKĞLKSAQCGSSIIXHCKHKLY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKG2-C type II integral membrane protein (NKG2-C activating receptor) (NK cell receptor C). KKC2 OR NKG2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83; Indels
λq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.8%; Score 162.5; DB 1
25.4%; Pred. No. 5.1e-09;
ive 28; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKGC_HUMAN STANDARD; PRT; 231 AA. P26717; 043802; Q9NR42; 01-AUG-1992 (Rel. 23, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91178434; PubMed=2007850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exp. Med. 173:1017-1020(1991).
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NCBI_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=NKG2-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLRC1 OR NKG2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKG2 genes.";
                                                                                                                                                                                                                                                                 RESULT 9
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                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                         NKG2 genes.";
J. Immunol. 168:240-252(2002).

J. Immunol. 168:240-252(2002).

L. FUNCTION: Plays a role as a receptor for the recognition of MHC class I HIA-E molecules by NK cells and some cytotoxic T-cells.

SUBGINIT: Can form disulfide-bonded heterodimer with CD94.

SUBGINIT: Natural killer cells.

TISSUE SPECIFICITY: Natural killer cells.

SIMILARITY: Contains I C-type lectin family domain.
                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANTS ASN-2 AND PHE-102.
MEDLINE-21623889; PubMed=11751968;
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
Sleland S., Guechlein L.A., Uhrberg M., Parham P.;
"Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
S -> N (in allele NKG2-C*02).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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S -> F (in allele NKG2-C*02).
/FTId=VAR_013405.
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                                                                                                                            Biassoni R.;
Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 602891; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005888; F:transmembrane receptor activity; TAS.
GO; GO:0006968; P:cellular defense response; TAS.
GO; GO:000165; P:signal transduction; TAS.
InterPro; IPR00136; Lectin_C.
Ffam; PF00059; lectin_C: 1.
SMART; SM00034; CLECT; 1.
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C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY
human natural killer gene complex.";
Immunogenetics 48:163-173(1998).
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EMBL, AJ001684; CAA04922.1; --
EMBL, Y13055; CAA73498.1; --
EMBL, AR260134; ARR86972.1; --
PIR; PT0374; PT0374
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MIM; 602891; -.
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231 AA;
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                                                                          SEQUENCE FROM N.A.
                                                                                                    IISSUE=Lymphoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
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DOMAIN
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SHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL-RNIDGWR 142
                        NKGA_PANTR STANDARD; PRT; 233 AA.

O95MIE; Q9MXM6;
28-FEB-2003 (Rel. 41, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating)
NK ceeptor) (NK cell receptor A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94. -!- SUBCELLULAR LOCATION: Type II membrane protein. -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P., "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS LEU-79 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                            ran trogicogres (chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20350666; PubMed=10894168;
Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
Parham P.;
                                                                               143 WE--GGPALSLRILINSLIQ-RCGAIHRNGLQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Rapid evolution of NK cell receptor systems demonstrated by comparison of chimpanzees and humans."; Immunity 12:687-698 (2000).
                                                                                                         184 WVIINGLAFKHKIKDSDNAELNCAVLQVNRLKSAQCGSSMIYHCKHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=095MIS-2; Sequence=VSP 003066;
-1- TISSUE SPECIFICITY: Natural killer cells.
-i- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
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EMBL; AF350005; AAK83792.1; -
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
NCBI_TaxID=88087;
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MEDIANE-9132000; PubMed=1831197;

Atoba H., Hyuga M., Morita T.;

"The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimerseurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein; terranctin, and lymphocyte Fc epsilon receptor for protein, terranctin, and lymphocyte Fc epsilon receptor for
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                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform NKG2-B) /FIId=VSP_003066.
                                                                                               EXTRACELLULAR (POTENTIAL). C-TYPE LECTIN (LONG FORM).
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N-LINKED (GLCNAC. .) (EN-LINKED (GLCNAC. .) (FOR N-LINKED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 220:382-387(1996).
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Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation update)
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MEDLINE=97331317; PubMed=9187649;
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MEDLINE=96184662; PubMed=8645314;
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01-NOV-1991 (Rel.
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10-OCT-2003 (Rel.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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cuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T., tructure of coagulation factors IX/X-binding protein, a heterodimer C-type lectin domains.";
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                                                                       Nat. Struct. Biol. 4:438-441 (1997).
-!- FUNCTION: Anticoagulant protein which binds with factor IX and factor X in the presence of calcium with a 1 to 1 stoichiometry.
-!- SUBURIT: Heterodimer of chains A and B; disulfide-linked.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANEOUS: Calcium is required for ligand binding.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COAGULATION FACTOR IX/FACTOR X-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 GPALSLRILINSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS050041; C TYPE LECTIN 2; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JC4691; JC4691.

PDB; 1IXX; 06-MAY-98.

PDB; 1BJ3; 16-AUG-99.

InterPro; IPR001304; Lectin C.

InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D83332; BAA11888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGRFIFMSFGFLVVFL
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1113
123
125
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135
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36
142
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Matches 39; Conserv
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SUBCELLULAR LOCATION: Type II membrane protein.

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X TISSUE-Blood, and Kidney;
A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Altasner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Joederg B., Buercw K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gubs R.A.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibs R.A.,
RA Richards S., Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Villalon D.K., Wuzny D.W., Sodergram B.J., Lu X., Gibs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Grenute B.N.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schenu J.E., Jones S.J.M., Marra M.A.;
RA Schnerch A., Schenu J.E., Jones S.J.M., Marra M.A.;
RA Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."; 6f more than 15,000 full-length
RT human and mouse cDNA sequences."; 6f more than 15,000 full-length
RT human and mouse cDNA sequences."; 6f more than 15,000 full-length
RT human and mouse cDNA sequences."; 6f more than 15,000 full-length
RT human and mouse cDNA sequences."; 6f more than 15,000 full-length
RT human and mouse cDNA sequences."; 6f more than 15,000 full-length
RT human and mouse cDNA sequences."; 6f more than 15,000 full-length
                                                                                                             D26715;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating NK receptor) (NK cell receptor A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plougastel B., Jones T., Trowsdale J.; "Genomic structure, chromosome location, and alternative splicing of
                                                                                                                                                                                                                                                                                                                                    MEDLINE=91178434; PubMed=2007850;
Houchins J.P., Yabe T., McSherry C., Bach F.H.;
"DNA sequence analysis of NKG2, a family of related cDNA clones
encoding type II integral membrane proteins on human natural killer
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kothapalli R., Kusmartseva I., Loughran T.P. Jr.; Identification and characterization of the NKG2A gene from large granular lymphocytic leukemia (LGL) cells."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plougastel B., Trowsdale J.;
"Sequence analysis of a 62-kb region overlapping the human KLRC
105 AAMLRYKAWAEESYCVYFKSTINNKWRSRACRMMAQFVCE 143
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B)
                                                                                                    233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          Exp. Med. 173:1017-1020(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96337918; PubMed=8753859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98260668; PubMed=9598306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunogenetics 44:286-291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 49:193-199(1998).
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the human NKG2A gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cluster of genes.
                                                                                                  NKGA HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAS.
TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 YORILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 NQGVKLFGEYLGQDFYWIGL-RNIDGWRW--EGGPALSLRILINSLIQ-RCGAIHRNGLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 EEEMKFLS--IISPSSWIGVFRNSSHHPWVTMNGLAFKHEIKDSDNAELNCAVLQVNRLK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SILIM 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0007166; P:call surface receptor linked signal transdu. .;
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein; Alternative splicing.
DOMAIN 70 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).

EXTRACELULAR (POTENTIAL).
C_TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 151; DB 1; Length 233; 23.0%; Pred. No. 7.2e-08; Live 29; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILM---
                                                                                                           IsoId=P26715-2; Sequence=VSP 003062;
TISSUE SPECIFICITY: Natural killer cells.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (in isoform NKG2-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1654BD7958C81A84 CRC64;
              Event=Alternative splicing; Named isoforms=2;
Name=NKG2-A;
IsoId=P26715-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         003062
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                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X54868; CAA38650.1; -
EMBL, U54786; AAB17133.1; -
EMBL, U54784; AAB17133.1; JOINED.
EMBL, U54785; AAB17133.1; JOINED.
EMBL, HC4785; AAB17133.1; JOINED.
EMBL, AF023840; AAC174881; -
EMBL, BC012550; AAB1253.1; -
EMBL, BC012550; AAH1250.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 AA; 26287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54867; CAA38649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 23.0%
les 45; Conservative
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:6374; KLRC1.
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231
130
229
221
102
103
151
113
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                                                                                         Name=NKG2-B;
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208
102
103
151
180
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DISULFID
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Matches
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47 TWADAEKFCTQQHTGSHLVSFHSTEEVDFVVFMTHQSLKSTFFWIGANNIWNKCNWQWSD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91349596; PubMed=1880421;
Glorda R., Trucco M.;
"Mouse NKR-Pl. A family of genes selectively coexpressed in adherent
"Jymphokine-activated killer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92388663; PubMed=1517565;
Giorda R., Weisberg E.P., Ip T.K., Trucco M.;
"Genomic structure and strain-specific expression of the natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR. B46467; B4646...
MGD; MGI:107539; Klrblb.
InterPro; IPR001304; Lactin_C;
InterPro; IPR001304; Lectin_C;
Pam; PR00059; lectin_C; 1...
PRINTS; PR0034; CLBCT; 1...
PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
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PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
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PROSITE; PS00611; C_TYPE_LECTIN_Z; 1...
PS00611; PS00611; C_TYPE_LECTIN_Z; 1...
PS00611; PS00611; C_TYPE_LECTIN_Z; 1...
PS00611; PS00611; C_TYPE_LECTIN_Z; 1...
PS00611; PS00611; PS00611; PS00611; PS00611; PS00611; PS00611; PS00611; PS00611; PS00611; PS00611; PS00611; PS0061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         killer cell receptor NKR-P1.";

J. Immunol. 149:1957-1963(1992).

-i- FUNCTION: May function as signal-transmitting receptor.

-i- SUBCELLULAR NOTATION: Type II membrane protein.

-i- TISSUE SPECIFICITY: Natural killer cells.

-i- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8D04C11DEBAB9C56 CRC64;
                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Matural Killer cell surface protein Pl-34 (NKR-Pl 34).
KLRBIB OR LYSSB OR LYSS-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 149; DB 1;
                                                                                                                                                                                                                                      223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunol. 147:1701-1708(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25157 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-29 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M77677; AAA39823.1;
EMBL; X64721; CAA45974.1;
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
169
186
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212
105
210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                      146 G 146
                                                                                                       G 107
                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
                                                                                                         107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                      NK12 MC
P27812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 DWNSSLKFCADK--GSHLLITFPDNQG----VKLFGEYLGQDFYWIGLRNI----DGWRWEG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGRRIFVSFGLL-VVFLSL-----SGSEAGFC-----CPSHWSSYDRYCYVFKQEM 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 LSRFAMVALGLLTVILMSLLMYQRILCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH C-104 IN ALPHA CHAIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
aggregating protein from Crotalus durissus terrificus venom.";
Blochem. J. 333:389-393 (1998)
-:- FUNCTION: Binds to the platelet and collagen receptor,
glycoprotein VI (GPVI).
-:- SUBUNIT: Heterohexamer of three alpha chains and three beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%; Score 150.5; DB 1; Length 148;
                                                                                                                                                                                                                                                                                                                                              Convulxin beta precursor (CVX beta).
Crotalus durissus terrificus (South American rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chains; disulfide-linked.
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                                                                                                                                                                                                                                                               (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONVULXIN BETA.
                                                                                                                                                                                                                 148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
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38; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINCE, SMOOD34; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PF00059; lectin_C; 1.
PRINTS; PR01504; PROCEATITSAP.
                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 B.
17402 MW;
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                                                              218 SAQCGSSIIYHCKHKL 233
                             172 ASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y16349; CAA76182.1; -. HSSP; P23807; 11XX.
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
26
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34
26
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Matches 38;
                                                                                                                                                                                                                 CRODU
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                                8
                                                                                                                                                     120 ADCGRKGATLLIODODEELRFLLDSIKEKYNSFWIGERFTLPDMNWKWINGTTFNSDVLK 179
                                                                                                                                  54 LM-----YQRILCCGSKDST----CSHCPSCPILWTRNGSHCYYFSMEKKDWNSSL 100
                                                                                                                                                                                                    101 KFCADKGSHLLTFPDNQGVKLFGEYLGQDF--YWIGLRNI---DGWRWEGGPALS---LR 152
                                                                RWKLKAVLHRPHLSRFAMVALGLLTVILMSL 53
                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 51:496-499(2000).
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC
-class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
-!- SUBCEDIULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LaBonte M.L., Levy D.B., Letvin N.L.; "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordatā; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-D type II integral membrane protein (NKG2-D activating NK
                              90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                      ILTNSLIQRCGAIHRNGLQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                           180 ITGDTENGSCASISGDKVTSESCSTDNRWICQKEL 214
              Pred. No. 1.1e-07; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20322487; PubMed=10866118;
22.8%; ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF190943; AAF74539.1; -.
InterPro; IFR001304; Lectin C.
Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor) (NK cell receptor D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Polymorphism.
                                                              6 IYSTLELPEAPQVQDES-
                            49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
213
110
211
211
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              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9544;
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98
99
127
189
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DISULFID
DISULFID
DISULFID
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              Best Local
Matches 4
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TISSUB-Pancreas, and Spleen;

WEDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

RIJORE R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Wallaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willand D.K., Muzup V.M., Sodergren E.J., Lu X., Gibbs R.A., Willand J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Reneration and initial analysis of more than 15,000 full-length human and mouse cDMA, sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGBYLGQDFYWIGLRNI---DGWRWEGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                           FIAVAMGIRFIIMVTIWSAVFLNSLFNQEV----QIPLTESYCGPCPKNWICYKNNCYQF
                                                                                                                                                                                                                                                                                                                                 --LMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYF
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-!- FUNCTION: Plays a role in B cell proliferation and differentiation. Associates with CDS.

-!- SUBDNIT: Homodimer; disulfide-linked.

-!- SUBCELLULAR LOCATION: Type II membrane protein.

-!- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(CLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDINE-90278102; PubMed=2141045; Von Hoegen I., Nakayama E., Parnes J.R.; Illiantification of a human protein homologous to the mouse Lybell differentiation antigen and sequence of the corresponding
                                                                                                                                                                                                     ; DB 1; Length 216; 1.3e-07;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                           A44883F31400DEAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 PALSLRILINSLIQR -- CGAIHRNGLQA--SSCEVALQWIC 183
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                                                                                                                                                                                                                                                                   65;
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01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
B-cell differentiation antigen CD72 (Lyb-2).
                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 AA
                                                                                                                                                                                                     14.4%; Score 148; 26.7%; Pred. No. 1
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N-LINKED
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131
163
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                                                                                                                                        216 AA;
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163
202
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                                             CARBOHYD
CARBOHYD
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                   CARBOHYD
                                                                                                              CARBOHYD
                                                                                                                                           SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTF----PDNQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 CGSAD-TC----CPSGWINHQKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSH 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 GVKLFGEYL----GQDFYWIGLRNIDGWRWEGGPALSIRILTNSLIQRCGAIHRN----G 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 SYYFLNSLLPNGGSGNSYWIGLSSNKDWKLIDD---IQRIRIYAQSSKCNKVHKIWSWWI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 EXTRACELLULAR (POTENTIAL).
352 C-TYPE LECTIN (LONG FORM).
354 BY SIMILARITY.
350 BY SIMILARITY.
342 BY SIMILARITY.
134 BY SIMILARITY.
135 N-LINKED (GLCNAC. . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                            MIM; 107272; -...
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:00155; P:cell adhesion; TAS.
InterPro; IPR001394; Lectin_C.
Ffam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615; CTYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein.
DOMAIN 1 95
CYTOPLASMIC (POTENTIAL).
differentiated plasma cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD72 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd72.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 LESESCRSSLPYICEMTAF 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 LQASSCEVALQWICKKVLY 188
                                                                                                                                                                                                                                     EMBL; M54992; AAA36189.1; -.
EMBL; BC030227; AAH3027.1; -.
PIR; A43532; A43532.
Genew; HGNC:1696; CD72.
MIM; 107272; --
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136
359 AA;
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Search completed: August 10, 2004, 16:17:00 Job time : 8.32035 secs

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(without alignments)
1819.059 Million cell updates/sec
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                                                                                              August 10, 2004, 16:11:32 ; Search time 32.6089 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 MADSSIYSTLELPEAPQVQD...
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sp_human:*
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sp_mammal:*
sp_mc:*
sp_nc:*
sp_organelle:*
sp_phage:*
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length: 2000000000
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Maximum DB seq
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

075613 homo sapien 043198 homo sapien 043198 homo sapien 0290536 gallus gall 091v25 mus musculu 054708 mus musculu 054707 mus musculu 052594 mus musculu 061973 mus musculu 061973 mus musculu 061973 mus musculu 061973 mus musculu 061973 mus musculu 061973 mus musculu 061974 macaca mula 088713 mus musculu Q64335 rattus norv Description SUMMARIES 088713 064335 075613 095613 0930636 091V25 091V25 091V25 091V25 091V25 091V25 0925G4 080CH7 0925G4 080CH7 0925G4 G 111111 DB Query Match Length 100.0 838 5568.5 568.5 548.5 180.5 180.5 179.5 177.5 177.5 177.5 1029 Score No. Result

Q8mji0 pongo pygma O8mji3 pongo pygma			Q9mzk3 macaca mula	Q8mi05 macaca fasc	Q8mjh8 pongo pygma	Q8mji4 pongo pygma		Q9gk88 macaca mula	Q802s8 gallus gall	Q8spx0 sus scrofa	Q9r007 mus musculu	Q8mjh5 pongo pygma				Q9nzs2 homo sapien	Q9mzk1 macaca mula		Q9iam0 agkistrodon	Q8jiw1 agkistrodon		Q95jg4 bos taurus			Q925g3 mus musculu	Q9mz39 pan troglod	Q96qp9 homo sapien
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Q8MJI0 O8MJI3	Q8MHY9	Q8SPX1	Q9MZK3	QBMI05	ОВМЛН8	Q8MJI4	TSZN60	Q9GK88	080258	Q8SPX0	Q9R007	Q8MJH5	Q8MJH9	Q8MJI1	Q9MZK2	O9NZS2	Q9MZK1	012918	Q9IAM0	QBJIW1	Q9UHP7	Q95JG4	O9GME8	Q9MZ40	Q925G3	Q9MZ39	Q96QP9
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233	179	200	231	231	233	179	181	231	200	159	165	233	233	233	246	231	246	225	146	146	191	161	233	233	223	226	334
17.0	17.0	17.0	17.0	16.8	16.7	16.7	16.7	16.6	16.5	16.4	16.3	16.3	16.3	16.2	16.2	16.2	16.0	16.0	15.9	15.9	15.9	15.8	15.8	15.8	15.7	15.7	15.7
175	174.5	174.5	174.5	173	172	171.5	171.5	170.5	169.5	169	168	168	168	167	167	166.5	165	164.5	163.5	163.5	163.5	163	162.5	162.5	161.5	161.5	161.5
17	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
SEQUENCE FROM N.A.
STRAIN=C.B-17 SCID;
MEDLINE=99077194; PubMed=8862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
"2F1 antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIR-129/SeverRefEr; TISSUB-Spleen;
MEDLINE-2115136; PubMed=11220622;
Voehringer D., Kaufmann M., Pircher H.;
VGenomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue of MARA.";
                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1999 (TrEMBLrel. 11, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                 Æ.
                                 188
                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 52:206-211(2001).
EMBL, AP097357; AAD03718.1; -.
EMBL, AOTO751; CAAD0342.1; -.
EMBL; AF317727; AAK40082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2-188 FROM N.A.
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1355294; Klrgl.
                                                                                                                                                KLRG1 OR MAFA.
Mus musculus (Mouse)
                                                                                                                                                                                                                    NCBI_TaxID=10090;
                           088713
RESULT 1
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us-09-811-367b-3.open.rspt

9 09

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MEDLINE=9907194; PubMed=9862378;
MEDLINE=99077194; PubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
It transmembrane receptor expressed by natural killer cells.";
It transmembrane receptor expressed by natural killer cells.";
Bull: A.F.09158; AAD03719.1; -.
REMBL; AF09158; AAD03719.1; -.
RO GO:0005529; Fsugar binding; IEA.
RO GO:0005529; Psugar binding; IEA.
REMBL; PR00059; lectin_c; 1.
REMBL; REMBL; REMONG34; Lectin_c; 1.
REMBL; REMBL; RESSO041; C. TYPE LECTIN 2; 1.
ROWSTTE; ROSO041; C. TYPE LECTIN 2; 1.
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                                                                                               61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                            121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSL-RILTNSLIQRCGAIHRNGLQASSCEVAL 179
                                                                              CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                          121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
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                                gene
                 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Butcher S., Arney K.L., Cook G.P.; MRFA-L, an ITIM-containing receptor encoded by the human NK cell complex and expressed by basophils and NK cells."; Eur. J. Immunol. 28:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ITIM-containing receptor MAFA-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.2%; Score 568.5; DB 4 57.2%; Pred. No. 2.3e-51; ive 25; Mismatches 54
                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                 189
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.2
Best Local Similarity 57.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 OWICKKV 186
                                                                                                                                                                                                        181 WICKKUL 187
                                                                                                                                                                                                                             WICEKUL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HWVCKKV 187
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                              61
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                      0;
                                                                                                                                                       100.0%; Score 1029; DB 11; Length 188; 100.0%; Pred. No. 1.5e-99; ive 0; Mismatches 0; Indels 0;
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80.7%; Pred. No. 1.5e-79;
ive 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] — SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAINSPRAGUE DAWLEY, TISSUE=Testis; Bocek Jr P., Guthmann M.D., Pecht I.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE=96016176, PubMed=7568140;
Guthmann M.D., Tal M., Pecht I.;
"A secretion inhibitory signal transduction molecule on
                                                                                                      PS50041; C_TYPE_LECTIN_2; 1.
188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005229; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001304; Lectin_C;
FMAR; FR00059; lectin_C; 1...
SMART; SM00034; CHECT; 1.
PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             another C-type lectin.,
Proc. Natl. Acad. Sci. U.S.A. 92;9397-9401(1995).
Broc. Natl. Acad. Sci. U.S.A. 92;9397-9401(1995).
Broc. Natl. X97191, CAA65829.1;
EMBL, X97193, CAA65829.1; JOINED.
EMBL, X97194, CAA65829.1; JOINED.
EMBL, X97195, CAA65829.1; JOINED.
EMBL, X79812; CAA56208.1;
PIR; 159421; 159421.
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InterPro; IPR001304; Lectin_C.
Pfam: PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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01-NOV-1996 (TrEMBLrel, 01
01-NOV-1996 (TrEMBLrel, 01
01-OCT-2003 (TrEMBLrel, 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.7
Matches 151; Conservative
                                                                                                                                                                                      Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         WICKKVLY 188
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                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAFA protein.
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SEQUENCE
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSL-RILINSLIQRCGAIHRNGLQASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                       1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to killer cell lectin-like receptor subfamily G, member
                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 195;
                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-Bone marrow;
TISSUB-Bone marrow;
Submitted (R.; 2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012621; AAH12621.1; -.
                                                                                                                                                                                                                                                                                                                                   195 AA; 21831 MW; 178EE98E08EEC473 CRC64;
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Last annotation update)
                                                                                                                                                                                                                           Genew; HGNC:6380; KIRG1...

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0005529; F:receptor activity; IEA.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007157; P:heterophilic cell adhesion; IEA.

InterPro; IPR00134; Lectin_C;

SMART; SM00034; CLECT; 1.

PROSITE; PS50041; C_TYPE_LECTIN_Z; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamers M.B., Lamont A.G., Williams D.H.;
"Human MAFA has alternatively spliced variants.";
Biochim. Biophys. Acta 1399:209-212(1998).
EMBL, AF034952; AAC34131.1,
                                                                                                                                                                                                                                                                                                                                                        54.9%; Score 564.5; DB 4; 57.0%; Pred. No. 6.1e-51; iive 25; Mismatches 54;
                                 195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mast cell function-associated antigen
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                                                       Created)
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                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 57.0
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                              (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 QWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 HWVCKK 186
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                                                                                                                                                                                                                                                                                                                        Lectin, Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                               NCBI_TaxID=9606;
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                096E93
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         RESULT 4
Q96E93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ILQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSL-RILTNSLIQRCGAIHRNGLQASSCEVAL 179
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                                                                                                           signal transdu. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bernot A., Zoorob R., Auffray C.;
"Linkage of a new member of the lectin supergene family to the chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Uniocen).
Eblarus gallus (Procent).
Archosauria, Avez, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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                                                                                                                                                                                                                                                                                                                                            Length 189;
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GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0003793; F:defense/immunity protein activity; TAS.
GO; GO:0005530; F:lectin; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0007166; P:cell surface receptor linked signal tra
GO; GO:0006968; P:cellular defense response; TAS.
InterPro; IPR001304; Lectin_C.
Pfam; PR00059; lectin_C; 1.
PFAM; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Indels
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InterPro; IPR002303; Attifreezell.
InterPro; IPR001304; Lectin_C.
Prints, PR00055; Jettin_C; 1.
PRINTS, PR000356; AUTTFREEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SRQUENCE 257 AA; 28814 MW; CG7EA483F4E85333 CRC64;
                                                                                                                                                                                                                                                              PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6_CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                         53.3%; Score 548.5; DB 4;
55.6%; Pred. No. 2.8e-49;
tive 26; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 AA
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PIR; IS0146; IS0146.
GO; GO:0005529; F:sugar binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mhc genes.";
Immunogenetics 39:221-229(1994)
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                            Matches 104; Conservative
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17.5.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 QWICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 HGVCKKV 187
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                      189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus.
NCBL_TaxID=9031;
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215

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:: | | | : | | | 11 TGDTENDSCAAISGDKVTFESCNSDNRWICQKELY
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6;
                                                                                                                KLRD1 OR CD94
                                                                            01-JUN-1998
                                                                                              -OCT-2003
                                                                                     01-JUN-1998
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             63
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                                                        054708
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                                     RESULT
                                              054708
ID 05
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                             RQNRRRVLCVALSAVPCMLVLALVAVIVLQRPSC--SPRPPFSHV ~- CPNAWVGFQGKCY 141
                  YFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG---WRWE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CG-----SKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHR-PHLSRFAM----VALGLLTVILMSLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FCADKGSHLLTFPDNQGVKLFGEYLGQDF--YWIGLRNI---DGWRWEGGPALS---LRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                           Kung S.K., Su R.C., Shannon J., Miller R.G.,
"The NKR-PlB gene product is an inhibitory receptor on SJL/J NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.5%; Score 180.5; DB 11; Length 227; 26.5%; Pred. No. 1.1e-10; ive 32; Mismatches 99; Indels 27;
                                                        145 GGPALSLRILTNSLI-----QRCGAIHRNGLQASSCEVALQWICKK 185
                                                                    | | : : | : : | : | : DGSA-----FINRPVFELRGGGRCAYLNGDGISSALCHSEKFWVCSR 243
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J;
Plougastel B.F.M., Yokoyama W.M.;
"Mouse NKR-PlA gene, genomic structure.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
NKR-PlA (Natural killer cell receptor protein NKR-PlA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 AA; 25715 MW; CCB8324AE07FBB97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 LTNSLIQRCGAIHRNGLQASSCEVALQWICKKVLY 188
                                                                                                                           ¥.
                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6;
MEDLINE=99248165; PubMed=10229823;
                                                                                                                                                                                                                                                                                                                                                 J. Immunol. 162:5876-5887(1999).
[3]
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SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                 KLRBIA OR NKR-PIA.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                  88
                                    142
                                                                          202
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                                                                                                                         Q91V25
Q91V25;
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Matches
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77 ILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGBYLGQDFYWIGL- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 ----RNIDGWRWEGGPALSLRILTN-SLIQRCGAI---HRNGLQASSCEVALQWICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YSEKRN--AWLWEDGTVPSKDLFPEFSVIRPEHCIVYSPSKSVSAESCENKNRYICKKL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKWVGHOCNCYFISKEEKSWERSRDFCASONSSLLQ-POSRNELSFMNF-SQTFFWIGHT
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                                                                                                                                                                                                                                                                                                            STRAINS—CB.NO. N.A.

STRAINS—CB.17 SCID.

X MEDLINE=98124458; PubMed=9464811;

MEDLINE=98124458; PubMed=9464811;

A Vance R.B., Tanamachi D.M., Hanke T., Raulet D.H.;

T. Cloning of a mouse homolog of C949 extends the family of C-type

I ectins on murine natural killer cells.";

EMBL; AR030312; AAC283441.;

R MGD; MGI:1196275; Klrd1.

R MGD; MGI:1196275; Klrd1.

R MGD; MGI:1196275; Edgar binding; IEA.

InterPro; IPR001309; Lectin.C.

R Pfam; PR00059; Lectin.C.

R SWART; SM0034; CLECTIN.Z; 1.

R PROSITE; PS00041; C TYPE LECTIN.Z; 1.

R PROSITE; PS00042; EGF 1: 1.
                                                                                                                                                                            Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
KIRDI OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 SRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20809 MW; D59E1CBB63139E45 CRC64;
                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.5%; Score 180; DB 11;
31.8%; Pred. No. 9.2e-11;
ive 25; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 AA
      Created)
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                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vance R.E., Tanamachi D.M., H
Eur. J. Immunol. 27:0-0(1997)
(TrEMBLrel. 06, C
(TrEMBLrel. 06, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Conservative
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153

27; Gaps

Indels

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61 LVRVLIQKPSIEKCYVLIQENLNKTTDCSAKLECPQDWLSHRDKCFHVSHVSNTWEKGLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||: |: |: |: |: |: |: |: ||1||
121 DCDGKGATIMLIQDQEELRFILDSIXEKYNSFWIGLRYTLPDMNWKWINGSTLNSDVLKI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 YORILC-----CG----SKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLK 101
                                                                                                                                                                                                                                                                                                                                                                                  1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHR-PHLSRFAM----VALGLLTVILMSLLIM 55
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDTARVYFGLKPPRTPGAWHESPPSLPPDACRCPRSHRLALKLSCAGLILLVVTLIGMSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 FCADKGSHLLIFPDNGGVKLFGEYLGQDF--YWIGLRNI---DGWRWEGGPALS---LRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MADSSIYSTLELPEAPQVQDESRWKL----KAVLHRPHLSRFAMVALGLL----TVILMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Giorda R., Weisberg E.P., Ip T.K., Trucco M.;
"Genomic structure and strain-specific expression of the natural
                                                                                                                                                                                                                                                       DB 11; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 17.4%; Score 179.5; DB 11; Length 227; Similarity 26.7%; Pred. No. 1.4e-10; 58; Conservative 33; Mismatches 95; Indels 31;
                                                                                                                                                                                         25767 MW; 18283316EADC6B13 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Natural Xiller cell receptor-Pl.
KIRBIA OR LYSSA OR NKR-Pl 2.
                                                                                                                                                                                                                                                 Query Match
17.4%; Score 179.5; DB 11;
Best Local Similarity 26.5%; Pred. No. 1.4e-10;
Matches 57; Conservative 32; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 LINSLIQRCGAIHRNGLQASSCEVALQWICKKVLY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TDDTENDSCAAISGDKVTFESCNSDNRWICQKELY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Æ.
                          Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  killer cell receptor NKR-Pl.";
J. Immunol. 149:1957-1963 (1992).
BNBL; K64716; CAA45971.1;
EMBL; K64717; CAA45971.1; JOINED.
BMBL; K64718; CAA45971.1; JOINED.
EMBL; K64724; CAA45971.1; JOINED.
HSSP; P22897; LEGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:107540; Klrbla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota, Metazoa,
                                                                                                                                                                                     227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 AA;
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Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                              Receptor.
                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         061973;
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                                 S K R R R S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 DKWVGHQCNCYFISKEEKSWKRSRDFCASQNSSLLQ-PQSRNELSFMNF-SQTFFWIGMH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 ILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 SRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDST-----CSHCPSCP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||:| :| :| :| TRWRLMSVIFGIK-CLFLMVTLG---VLLINSFTIQNIQSTPSPTTTVBFQEVSECCVCL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----RNIDGWRWEGGPALSLRILTN-SLIQRCGAI---HRNGLQASSCEVALQWICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YSEKRN--AWLWEDGTVPSKDLFPEFSVIRPEHCIVYSPSKSVSAESCENKNRYICKKL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Mammary gland;
Butcher S., Cottage A., Cook G.P.;
"Mouse natural killer cell receptors homologous to human CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kung S.K., Su R.C., Shannon J., Miller R.G.; "The NKR-PlB gene product is an inhibitory receptor on SJL/J NK
STRAIN=CS7BL/6J;
Heusel J.W., Ho E.L., Brown M.G., Matsumoto K., Yokoyama W.M.;
"Murine CD94.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75; Indels
                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, AF030311, AAC2843.1; -.

EMBL, AF030025, AAC33713.1; -.

EMBL, AF057714; AAC33713.1; -.

MGD, MGI:1196275, Klrdl.

GO, GO:0005529; F:sugar binding; IEA.

GO, GO:000757; P:heterophilic cell adhesion; IEA.

InterPro; IPR006209; EGF_like.

InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kung S.K.P., Su R.C., Shannon J., Miller R.G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF354261; AAK39101.1; -. GO; GO:0004872; F.receptor activity; IEA. GO; GO:000529; F.sugar binding; IEA. InterPro; IPR002353; AntifreezeII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 AA; 20808 MW; DD343419E93B3465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Natural killer cell receptor protein NKR-PIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%; Score 180; DB 11; 31.8%; Pred. No. 9.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Mismatches
                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SJL/J;
MEDLINE=99248165; PubMed=10229823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunol. 162:5876-5887(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 31.8
les 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SJL/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells.";
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0925G4 RESULT 10

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31; Gaps

09

53

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56 YORILCCGSKDSTCSHCPSCPILWTRNGSHCYYPSMEKKDWNSSLKPCADKGSHLLTFPD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 NQGVKLFGEYLGQDFYWIGL-RNIDGWRWE--GGPALSLRILTNSLIQR-CGAIHRNGLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 EEEMKFLGTILPSS--WIGVFRNSSHHPWVTINGLAFKQEIKDSDNAEHDCAVLHTRGLR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----STTW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KLIVGILGIICLVLMASVVTIVVIPSTLIQ 99
                                                                                                        MEDLINE=222772192; PubMed=12077248; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; Mr Cell Receptors of the Orangutan (Porgo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 KHNSSSLNTRTQKAHRCGHCPEEWITYSNSCYYIGKEKRTWEESLLACASKNSSLLSIDN
                            Eukāryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LaBonte M.L., Letvin N.L.;

"Analysis of rhesus monkey CD94/NKG2 family members.";

Submitted (JUN-2011) to the EMBL/GenBank/DDBJ databases.

EMBL, AF395617, AAK97464.1, -.

GO; GO:0005529; F:sugar binding; IEA.

InterPro; IPR001304; Lectin C.

Pfam; PF00059; lectin C: 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN L; 1.

PROSITE; PS00615; C_TYPE_LECTIN L; 1.

SROUNCE 236 AA; Z6365 MW; I987FABF3641351E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 YSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILM----
                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Indels
                                                                                                                                                                                                                                                                                                                                                                     233 AA; 26239 MW; 6B8AE8489BAD2686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                               J. Immunol. 169:220-229(2002).

EMBL; AR47035; ARM78455.1, -.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:000757; P:heterophilic cell adhesion; IEA.

InterPro; IPR001304; Lectin_C.

Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    17.2%; Score 177; DB 6; 24.5%; Pred. No. 2.6e-10; ive 28; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 AA
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 ASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 SNKCGSSILYHCKHKL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, (TrEMBLrel. 25,
            Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 YHCKDLPSAPE---
                                                                                                                                                                                                                                                                                                                       SMART; SM00034; CLECT
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                            NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q95L94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                 151
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                                     85 HCYYPSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPDIELQKDSDC--C-SCQEKWVGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22072192; PubMed=12077248; GuethLein L.A., Flodin L.R., Addms E.J., Parham P.; Mcell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
              LMYQRILC-----CG----SKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSS
                                                                                 LKFCADKGSHLLTFPDNQGVKLFGEYLGQDF--YWIGLRNI---DGWRWEGGPALS---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWENGSALSQYLFPLFETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 RWEGGPALS---LRILTNSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 177.5; DB 6; Length 179;
; Pred. No. 1.7e-10;
16; Mismatches 69; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;
                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT'2002 (TrEMBLrel. 22, Created)
1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell lectin-like receptor.
                                                                                                                                                                    152 RILINSLIQRCGAIHRNGLQASSCEVALQWICKKVLY 188
                                                                                                                                                                                                                                                                    179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol. 169:220-229(2002).

EMBL, AF470381; AAM78481.1; -.

EMBL, AF470382; AAM78482.1; -.

GO; GO:0004872; F: receptor activity; IEA.

GO; GO:0005529; F: segar binding; IEA.

InterPro; IPR00509; EGF like.

InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS50041; C TYPE LECTIN 2; 1. PROSITE; PS00022; EGF 1; 1.
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 GLLTVILMSLLMYQRILCCGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.2%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31...
Local Similarity 31...
                                                                                                                                                                                                                                                                                                                                                                                       Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with MHC-C.";
                                                                                                                                                                                                                                                                                                                                                                       POPY-CD94.
                                                                                 100
                                                                                                                                                                                 179
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                                                                       7;
                                                                                                                                                                      :: | :| | | : | | | 55 NDKTYHCKGLLPPP--EKLTAEVLGIICIVLMATVLKTVVLIPCIGVLEQNNFSINTRIQ 112
                                                                                                                                                                                                                                                                                                       113 KAYDCGHCPEEWITYTUS---CYYIGKEKRTWEESLLITCASKUSSLLSIDNEEEMQLLGS 169
                                                                                                                                                                                                                                                                                                                                                                                            125 YLGODFYWIGLRNIDG---WRWEGGPALSIRILTNSL-IORCGAIHRNGLOASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                        |--SVLSWVGVSRSSSDHPWVSINGSTFKLKIAESDIGKENCVMLHSSGLKSHRCGASQL 227
                                                                                                                                                                                                                                                              65 KDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGE 124
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                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                       26;
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17.2%; Score 177; DB 6; Length 236; 25.0%; Pred. No. 2.6e-10; ive 33; Mismatches 82; Indels
                                                                                                                             20 DESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL--CCG-
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275 AA; 31360 MW; C9792BA25C8B5CC2 CRC64;
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31.7%; Pred. No. 3.1e-10;
iive 17; Mismatches 57;
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GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin.C.
Fran; PF00059; lectin.C; 1.
SWART; SM00034; CLECT; 1.
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STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-21085660; Pubmed-1121781;
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4933425B16RIK.
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Best Local Similarity
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57; Indels

40; Conservative

Matches

Local Similarity

72 CPSCPILMTRNGSHCYYFSM-EKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQ-- 128

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129 DFYWIGLR-NIDG--WRWEGGPALSLRILTNSLI-----QRCGAIHRNGLQASSCEVAL 179
                                                           199 SFFWLGLSWNSSGRNWLWEDGSFPPPTLLSDKELASFNGSRECAYFERGNIYTSRCRAEI
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-811-367B-3 1029

1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 score: Title: Perfect :

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp1980s:* geneseqp2000s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* Geneseq 29Jan04:* 7: 8 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	scription	Aae11760 Mouse mas	Aar77033 Mammalian	Aaw88277 Rat mast	Aae11761 Rat mast	Add25635 Binding d	Aar77472 Partial s	Aaw88265 Human mas	Aae11759 Human mas		Abj37898 NOVX prot		Aaw85594 Chicken 1	Aaw64791 Human Kp4	Aaw40222 CD94. 7/1	-	Aar54659 Human CD6	m	Add25621 Binding d	Abb80569 Human sbq		Aar54660 Murine CD	Aaw85595 Mouse CD6	Aam80296 Human pro		2 Human
SUMMAKIES	QI	۱ ۲	AAR77033	AAW88277	AAE11761	ADD25635	AAR77472	AAW88265	AAE11759	ABG05451	ABJ37898	AAW88267	AAW85594	AAW64791	AAW40222	ADE76965	AAR54659	AAW85593	ADD25621	ABB80569	ABB81897	AAR54660	AAW85595	AAM80296	ABG72616	AAM80302
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o k	Query Match	100.0	81.4	81.4	81.4	55.2	53.5		53.3	40.9	26.0	21.6	17.7	17.3	17.3	17.3	16.9	16.9	16.9	16.8	16.7	16.3	16.3	16.3	16.3	16.3
	Score	1029	838	838	838	568.5	551	548.5	548.5		267.5	222.5	182	178.5	178.5	178.5	173.5	173.5	173.5	172.5	171.5	168	9		167.5	
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ALIGNMENTS

Mouse mast cell function associated antigen (MAFA) protein. AAE11760 standard; protein; 188 AA. (first entry) 18-DEC-2001 AAE11760; RESULT 1 AAE11760

Mouse, pharmaceutical composition, mast cell function associated antigen, MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.

Mus sp

64. .188 /note= "Extracellular domain" Location/Qualifiers Key Domain

WO200170805-A2

27-SEP-2001

16-MAR-2001; 2001WO-US008596.

17-MAR-2000; 2000US-0190716P.

(GEMI-) GEMINI SCI INC.

Ë Takahashi N, Mikayama WPI; 2001-611482/70. N-PSDB; AAD18735.

Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.

Example 1; Page 19; 49pp; English.

The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (WAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical

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composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic treating a T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is mouse MAFA protein
                                                                                                                                                                                                                                                                                                                                     CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                      LFGEYLGQDFYWIGLRNIDGRRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                  MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVIIMSLLMYQRIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in
                                                                                                                                                                                                                                                     1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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                                                                                                                                                                                    100.0%; Score 1029; DB 4;
100.0%; Pred. No. 6.6e-103;
live 0; Mismatches 0;
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                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guthmann MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WICKKVLY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WICKKVLY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-366356/47.
                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT01471.
                                                                                                                                                       Sequence 188 AA;
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(RYCU/) RYCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus rattus
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                                                                                                                                                                                                                   188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prevention
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                                                                                                                                                                                CGGSKGFMCSQCSRCPNLWARNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
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                                                                                                                                                                CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                   LFGEYLGODFYWIGLRNIDGWRWEGGPALSLRILTWSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of rat mast cell function-associated antigen (MAFA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFA molecule (see AAW82265) and to the discovery of splice variants (see AAW88266-67) of human MAFA that are not found in rat. Polypeptides and synthetic
combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                             1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVWVALGLLTVILMSLLLYQRTL
                                                                                                            1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rat;
therapy.
                                                                                   Gaps
                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mast cell function-associated antigen; MAFA; splice variant; inflammation; allergy; asthma; rheumatoid arthritis; tumour;
                                                      Length 188;
                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat mast cell function-associated antigen (MAFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams DH;
                                                        Score 838; DB 2;
Pred. No. 3.2e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32. .84
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Asn is N-glycosylated"
                                              81.4%; Scc...
80.7%; Pred. No. 5...
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lamont A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       AAW88277 standard; protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-GB001572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, and tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lamers MBAC,
                                                                                                                                                                                                                                                                          WICKKUL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-059806/05.
N-PSDB; AAV84222.
                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                      Similarity
                                                                                                                                                                                                                                                                                           WICEKVL 1
                                Sequence 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-DEC-1998,
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                                                                                   151;
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                                                        Query Match
                                                                         Local
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Matches
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                                                                                                                                                                                                                                                                                                                                  CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                             CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILINSLIQRCGAIHRNGLQASSCEVALQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
peptides (see AAW88258-64) based on human MAFA and human truncated MAFA, and polynucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
                                                                                                                                                                               MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                           MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLITVILMSLILYQRTL
                                                                                                                                                    Gaps
                                                                                                                                                    ·.
                                                                                                                    Length 188;
                                                                                                                ; Score 838; DB 2; Length 18; Pred. No. 3.2e-82; 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mast cell function associated antigen (MAFA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE11761 standard; protein; 188 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; cytostatic.
                                                                                                                    81.4%;
80.7%;
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                                                                                                    Query Match
Best Local Similarity 80.7%
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                                                                                                                                                                                                                                                                                                                                                                               WICKKVL 187
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N-PSDB; AAD18736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001
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                                                                                   Sequence
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to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface NARA binding to the ligand on the target cell. The agent or the composition is useful for treating tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic received by stimulating the cytotoxic activity of an NK cell or a cytotoxic tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MAFA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding domain; immunoglobulin; fusion protein; cytostatic;
antiarthritic; immunosuppressive; antidiabetic; antithyroid;
neuroprotective; hinge region; immunoglobulin heavy chain;
CH2 constant region; CH3 constant region; IgG1;
antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNOGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding domain-immunoglobulin fusion protein-associated protein #95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                       Length 188
                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
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                                                                                                                                                                                                                                                                                                                       81.4%; Score 838; DB 4;
80.7%; Pred. No. 3.2e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thompson
                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD25635 standard; protein; 189 AA.
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2002US-00053530.
2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WICKKVL 187
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                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                                            Sequence 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003118592-A1
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17-JAN-2002;
03-JUN-2002;
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                                                                                                                                                                                                                                                                                                                           Query Match
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      8X363333XX
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Partial sequence of mast cell function-associated antigen (MAFA).

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comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin havy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the CH2 constant region polypeptide that is fused to the CH2 constant region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide contains of mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains the mutated human IgG1 immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin fusion protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple solerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CQGSNYSTCASCPSCPDRWMKYGNHCYYPSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LFGEYLGODFYWIGLRNIDGWRWEGGPALSL-RILTNSLIQRCGAIHRNGLQASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of at least one immunological activity comprising antibody dependent cell-mediated cytocoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and is also available in electronic format directly from USPTO at seqdata uspto.gov/sequence.html?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
                      invention relates to a binding domain-immunoglobulin fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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HWVCKKV 187
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75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG 134
                      Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
                                                                                                                                                                                                                                                                                                                                                                                                      A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand-screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                     Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mast cell function-associated antigen; MAFA; splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.5%; Score 551; DB 2; Le
llarity 84.1%; Pred. No. 1.9e-51;
Conservative 9; Mismatches 9;
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137. .139
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/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                   of inflammatory and allergic reactions.
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                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 38; 54pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW88265 standard; protein; 189 AA.
                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD. (RYCU/) RYCUS A.
                                                                                                                                                             95WO-US004258.
                                                                                                                                                                                     94IL-00109257.
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                                                                                                                                                                                                                                                         Guthmann MD,
                                                                                                                                                                                                                                                                                  WPI; 1995-366356/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 95; Conserv
                                                                                                                                                                                                                                                                                               N-PSDB; AAT01471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 114 AA;
                                                                              Rattus rattus.
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                                                                                                                                                            06-APR-1995;
                                                                                                                                                                                       08-APR-1994;
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                                                    prevention.
                                                                                                                                                                                                                                                         Pecht I,
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Novel human diagnostic protein #5442.
    immunosuppressive; cytostatic.
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                                                                                                                                                                                                                                                                                                This is the amino acid sequence of human mast cell function- associated antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198) encoding human MAFA can be obtained from myelogenous leukaemic cell line KU812 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW88277) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (TIMM) and an extracellular lectin-like domain. 2 Alternatively spliced forms (see Synthetic peptides (see AAW88258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth
                                                                                                                                                                                                                     New polypeptide having a sequence corresponding to human mast cell function-associated antipen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLV1TDNQEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGSKDSTCSHCPSCPILWTRNGSHCYYPSMEKKDWNSSLKPCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFGEYLGQDFYWIGLRNIDGWRWEGGPALSL-RILTNSLIQRCGAIHRNGLQASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, pharmaceutical composition, mast cell function associated antigen, MAFA; natural Killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human mast cell function associated antigen (MAFA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.3%; Score 548.5; DB 2;
55.6%; Pred. No. 7e-51;
live 26; Mismatches 56;
                                                                                                                                                              Williams DH;
/note= "Asn is N-glycosylated"
150. .152
/note= "Asn is N-glycosylated"
                                                                                                                                                               Lamont A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE11759 standard; protein; 189 AA.
                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 44pp; English.
                                                                                                                                      (PEPT-) PEPTIDE THERAPEUTICS LTD
                                                                                                                 97GB-00011148,
                                                                                          98WO-GB001572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 55.6 es 104; Conservative
                                                                                                                                                              Lamers MBAC,
                                                                                                                                                                                     WPI; 1999-059806/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QWICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 HGVCKKV 187
                                                                                                                                                                                              N-PSDB; AAV84198
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 189 AA;
            Modified-site
                                             WO9854209-A2
                                                                                          29-MAY-1998;
                                                                                                                 31-MAY-1997;
                                                                   03-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated an attent (MK) - or T-cell-expressed cell; and prevents or inhibits natural killer (MK) - or T-cell-expressed cell surface MAPA from binding to MAPA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAPA composition in vitro, ex vivo or in vivo by administering the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in a manount sufficient to inhibit cell surface MAPA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is human MAPA protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKPCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSL-RILTNSLIQRCGAIHRNGLQASSCEVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MADSSIYSTLELPEAPQVQDESRWKLKAVIHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.3%; Score 548.5; DB 4;
55.6%; Pred. No. 7e-51;
live 26; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG05451 standard; protein; 843 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 18; 49pp; English.
                                                                                                                                                                                                   16-MAR-2001; 2001WO-US008596.
                                                                                                                                                                                                                                                                      17-MAR-2000; 2000US-0190716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6%
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          Takahashi N, Mikayama T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-611482/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HGVCKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD18734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 189 AA;
                                                               WO200170805-A2
                                                                                                                                                                                                                                                                                                                                          GEMINI
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                   27-SEP-2001
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ij

9 09 NOVX protein sequence SEQ ID No 42.

(first entry)

22-MAY-2003

ABJ37898;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (I) and its binding partners are useful in medical imaging of sites expressing (II) (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are responsible for general social social sequences have applications and polynersity are assessed as a product of a session of mutations and polyneric diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 HCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  725 SCPSCPDRWMXYGNHCYYFSVEEKDMNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAF 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                    Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement; medical imaging; diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CWIGLRNNSGWRWEDGSPINFSRNTNGTIIRKRKHLHKN 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 YWIGLRNIDGWRWEGGPALSLRILTN-SLIORCGAIHRN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 35810; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
                                                                                                                                                                                                                                                                                       23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity.
                                                                                       Homo sapiens.
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ABJ37898 standard; protein; 191 AA.

RESULT 10 ABJ37898

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Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer; vulnerary; virucide; antibacterial; protozoacide; fungicide; noctropic; antiparstitc; neuroprotective; cerebroprotective; antiparkinsonian; anticonvulsant; antiadictive; analgesic; dermatological; keratolytic; antiseborrheic; antiathrutuc; antiarthrutuc; antiinflammatory; anti-HIV; cytostatic; antiasthmatic; antiathrutuc; hypotensive; osteopathic; neuroleptic; antidepressant; antidabetic; antiallergic; hammostatic; neuroleptic; antidepressant; antiinflammatory; human disease; NOVX-associated disorder; transma, viral; bacterial; fungal; protozoal; parastitic infection; Alzheimer's dieease; stroke; forensic biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gusev V;
Boldog F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides, designated as NOVX, useful for diagnosing and treating infections, neurological diseases, cancer, allergy, and bone, immunological, skin, renal, brain, muscle and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decristofaro MF, Padigaru M, Miller C, Tchernev V, Zhong H; Zhong M, Anderson D, Ballinger R, Gerlach V, Spytek KA, Rastel Kekuda R, Guo X, Zerhusen B, Andrew D, Mezes P, Patturajan M; Burgess CE, Eisen A, Wolerc A, Baumgartner J, Shimkets RA, Gus Vernet CAM, Taupier RJ, Pena C, Shenoy S, Li L, Casman S, Bol Fernandes E, Smithson G, Malyankar U, Taillon B, Liu X;
                                                                                                                                                                                                                                                 immunogen; non-human transgenic animal; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 118; 672pp; English
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2001US-0287484P.
2001US-0291701P.
2001US-0296960P.
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2001US-0275927P.
2001US-0275990P.
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2001US-0279857P.
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2001US-0304355P.
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2001US-0330227P.
2001US-0334198P.
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2001US-0264139P.
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2001US-0263351P.
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2001US-0277358P.
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2001US-0263799P.
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                                                                                                                                                                                                                                                                                                                                                                22-JAN-2002; 2002WO-US002064
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                                                                                                                                                                                                                                                                                                        WO200281517-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2001;
15-MAR-2001;
23-MAR-2001;
23-MAR-2001;
29-MAR-2001;
20-APR-2001;
20-APR-2001;
                                                                                                                                                                                                                                                                           Unidentified.
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14-MAR-2001;
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10-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2001;
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Mast cell function-associated antigen; MAFA; huMAFA(E3/4-);

splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

Homo sapiens WO9854209-A2

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The invention relates to a novel isolated polypeptide, designated NOVX (NOV1 - 13), consisting of a mature form of one of 61 sequences, given in the variant differ from the mature form, provided that the variant differs in the variant differ from the mature form, provided that the variant differs in the variant differ from the mature form, provided that the variant differs in the ward of the mature form, provided that the variant differs in the mature form. The NOVX polypeptides, are useful for treating a syndrome associated with a human disease (NOVX-associated disorder in humans and for treating a syndrome associated with a human disease (NOVX-associated disorder). NOVX polypeptides and the modifier acids, are useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX predisposition to a disease associated with altered levels of NOVX predisposition to a disease associated with altered levels of NOVX collapseptide as also useful for identifying an agent that binds to NOVX and a cell expressing NOVX is useful for identifying an agent that binds to NOVX collapseptide having 95 % sequence identity to NOVX polypeptide are useful for teating or not predisposed to the disease. NOVX collapseptides are useful for teating or preventing disorders are also useful for determining the presence or amount of NOVX in a sample. NOVX collypeptides are useful for treating or preventing disorders or syndromes including trauma, viral, bacterial, fungal, protectoral, and parabiler infections. They can also treat disorders such as e.g., Alzheimer's infections they can also treated disorders such as e.g., Alzheimer's collypeptides are useful for treating or preventing disorders are also useful for identifying and/or coloning NOVX monologues in other cell represence or a stroke. The NOVX encounts of NOVX sequences are also useful for identifying and/or coloning now prove the sequence of an indentifying and/or cloning NOVX monologues in other cells or produced and modulating NOVX activi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. The NOVX nucleic acids can be used in gene therapy. This sequence represents a NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids can be used in gene therapy. This sequence represents a NOVX protein of the invention
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to human mast cell and manufacturing inflammatory and allergic

New polypeptide having a sequence corresponding function-associated antigen - useful in forming pharmaceutical compositions in the treatment of

Disclosure; Fig 3; 44pp; English.

This is the

antigen

diseases, and tumour growth.

Williams DH;

Lamont A,

Lamers MBAC,

EL,

Hewitt

WPI; 1999-059806/05.

N-PSDB; AAV84200

(PEPT-) PEPTIDE THERAPEUTICS LTD

98WO-GB001572.

29-MAY-1998;

03-DEC-1998.

Truncated MAFA polypeptides including huMAFA(E3/4-), and polymucleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and

is the amino acid sequence of human mast cell function- associated gen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-domain of human MAFA (see AAW88265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail 9 9 63

71 HCKICEPCPTSWLPFGGSCYYFSVPKTTWAEAQGHCADASAHLAAFFEDRKVAFYSVLLG 130 68 TCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLG 127 LPEAPQVQDESRWKLXAVLHRPHLS----RFAMVALGLLTVILMSLLMYQRILCCGSKDS 67 LPESPOFESHORLVLLPIL-EIHVNSKSYRMYSFCLGFLTLVRQSLALSPRLECSGAISA 70 Gaps 23; DB 6; Length 191; Indels ODFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHR---26.0%; Score 267.5; DB 6; 31.2%; Pred. No. 1.9e-20; ive 27; Mismatches 80; Similarity 31.2 59; Conservative 182 KWWHCSKTL 190 LQWICKKVL 187 Sequence 191 AA; 179 Query Match Best Local S 12 12 128 Matches qq a δ g ð g ò à

Human MAFA splice variant huMAFA(E3/4-).

(first entry)

29-MAR-1999

axaxaxax

AAW88267

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AAW88267 standard; protein; 99

RESULT 11 AAW88267

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61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                               121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                         1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                   1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSRPSCSCLVAIALGLLTAVLLSVLLYQWIL
                                                                                                                                                                                                                                                                                                                    89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lectin; carbohydrate; binding; agglutination; selectin; receptor;
                                                                                                                                                                                                                                                                                                       Length 99;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                       Score 222.5; DB 2; Pred. No. 5.9e-16; 13; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW85594 standard; protein; 257 AA.
                                                                                                                                                                                                                                                                                                       21.6%;
30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                         asthma), or tumour growth
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              181 WICKKV 186
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                                                                                                                                                                                                                                                                                        Sequence 99 AA;
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02-MAR-1999
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AAW85594
셤
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us-09-811-367b-3.open.rag

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cell-mediated cytotoxicity; transplant rejection; autoimmune disease.
                                                                                                                                                                                                          Lopez-Botet M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW40222 standard; peptide; 179 AA
                                                                                                                                                                                                                                                                                                            Claim 1; Col 31-32; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 GLLTVILMSLLMYQRILCCGS--
                                                                                                      96US-00650578.
                                                                                                                              93US-00175339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US013077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-00690095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Conservative
                                                                                                                                                                    LOPEZ-BOTET M.
                                                                                                                                                       SCHERING CORP
                                                                                                                                                                                                           Lanier LL, Chang C,
                                                                                                                                                                    (LOPE/) LOPEZ-BOTET (BELT/) BELTRAN J A.
                                                                                                                                                                                                                                WPI; 1998-530877/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    or therapeutic use
                                                                                                                                                                                                                                               N-PSDB; AAV46476
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 179 AA;
                             Homo sapiens,
                                                                                                      20-MAY-1996;
                                                                                                                              29-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9804585-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-1996;
                                                                              22-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW40222;
                                                                                                                                                       (SCHE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                            Chicken 17.5.3 protein shows homology with the human CTL-1 protein.

Recombinant cells containing expression vectors comprising the CTL-1
coding sequence can be used to produce recombinant CTL-1 which is useful
for traising Ab and to screen for specific binding agents. Binding agents
which are antagonists of CTL-1 can be used to treat or prevent cancer,
e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are
associated with overexpression of CTL-1. Fragments of this sequence are
used to diagnose these conditions, as probes or primers in usual
hybridisation and/or amplification assays, or for gene mapping, while
complements of this sequence, antisense or ribozyme sequences are used to
treat or prevent the aforementioned cancers also. Ab are used directly as
antagonists or for delivery of therapeutic agents to cells that express
CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) and
also a transmembrane domain, but no secretory signal. CTL-1 also shows
homology with human CD69 (AAM85593), and mouse CD69 (AAM85595) proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG---WRWE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calcium dependent binding; treatment; cancer; detection; identification; CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor;
                                                                                                                                                                                                                                                       New human C-type lectin and related nucleic acid, vectors, transformed cells - antibodies, agonists and antagonists, for diagnosis, prevention and treatment of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 RPHLSRFAMVALG----LLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGSA----FTNRPVFELRGGGRCAYLNGDGISSALCHSEKFWVCSR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPALSLRILINSLI-----QRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 182; DB 2; Length 257;
; Pred. No. 5.1e-11;
25; Mismatches 72; Indels ;
                                                                                                                                                                                                                                                                                                         Example 3; Page 48-49; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 179 AA.
                                                                                                                98WO-US008791
                                                                                                                                        97US-00846523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.78;
28.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Conservative
                                                                                                                                                                (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                 WPI; 1999-024060/02
                                                                                                                                                                                          Shah P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Kp43 protein.
                                                                                                                                                                                                                                N-PSDB; AAV83109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 257 AA;
                                     gallus.
                                                                                                                                        29-APR-1997;
                                                              WO9849306-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1998
                                                                                      05-NOV-1998
                                                                                                                                                                                           Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW64791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
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                                     Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      datches
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                              This sequence represents a novel human natural killer (NK) cell surface antigen, Kp43. This sequence can be used in a method resulting in the production of recombinant protein expressed by NK and T cells, which may inhibit cell-mediated cytotoxidity, e.g. in transplant rejection or autoimmune diseases, or may be used to produce antibodies for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC 70
                                                                                                                                                       DNA encoding natural killer cell surface antigen Kp43 - and transformed cells for producing recombinant Kp43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phillips JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 RWEGGPALSLRILIN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMAH; apoptosis; osteoarthritis; diagnosis; treatment.
Beltran JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 178.5; DB 2;
; Pred. No. 7.5e-11;
17; Mismatches 68;
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Claim 1; SEQ ID NO 130; 41pp; English.

disorders.

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Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                             human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein expressed in a liver disorder #36.
                                                                                                                                                                                                                                                                                                                                                                          ADE76965 standard; protein; 179 AA
                        Goli SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000US-0222113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2001; 2001US-00919039.
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                      54; Conservative
                         Hillman JL, Au-Young J,
       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-031227/03.
                                          WPI; 1998-130617/12
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KASE/) KASER M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADE76964
                                                                                                                                                                                   Sequence 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaser MR;
                                                                                                                                                                                                                                                                                                                                                                                            ADE76965;
                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                          RESULT 15
ADE76965
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The invention relates to a composition comprising several CDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type for treating liver disorder such as hyperlipidaemia, hypertension, type compounds to identify a ligand which specifically binds a CDNA. A protein encoded by the CDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify a ligand which specifically binds the compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the CDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition is useful for detecting and composition and composition is useful for detecting and composition and composition is useful for detecting and composition and composition and a composition and a push and a composition encoded by a cDNA differentially expressed in a
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The type II integral membrane proteins (AAW40219-W40221) and CD94 (AAW40222) form a group which has 20% homology with the human macrophage antigen (TWAH) (AAW40215). The homology which TWAH shares with this group includes a series of disulphide residues. The structural homology between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GTLGIICLSIMATLGILLKNSFTXLSIEPAFTPGPNIELQKDSDC--C-SCOEKWGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                          Human macrophage antigen - used for decreasing apoptosis associated with osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the peptides provides information on the structural and physical properties of both the TMAH gene and protein. This is used in the development of TMAH as a diagnostic tool and as a method of treating diseases associated with expression of TMAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWEGGPALSLRILIN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.3%; Score 178.5; DB 2; Length 179; 31.8%; Pred. No. 7.5e-11; ive 17; Mismatches 68; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 47; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 GLLTVILMSLLMYQRILCCGS-
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Sequence 179 AA; liver disorder

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7;
                                                                                                                                          85 HCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                    1 NCYFISSERKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                       84
                                                                                                        70
                                                                                                      14 GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCOEKWVGYRC
                                                                       -- KDSTCSHCPSCPILWTRNGS
                                     31; Gaps
                                                                                                                                                                                                                   142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALOWICKKVL 187
                                                                                                                                                                                                                                                     129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
Length 179;
                                   Indels
17.3%; Score 178.5; DB 8;
31.8%; Pred. No. 7.5e-11;
iive 17; Mismatches 68;
                                                                          44 GLLTVILMSLLMYQRILCCGS-
                                         54; Conservative
     Query Match
Best Local Similarity
                                           Matches
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 3, Appli	Sequence 5, Appli	Sequence 196, App	Sequence 1, Appli	Sequence 4, Appli	Sequence 130, App	Sequence 10, Appl	Sequence 86, Appl	Sequence 182, App	Sequence 3, Appli	Sequence 26, Appl	Sequence 1, Appli	Sequence 158, App	Sequence 160, App	Seguence 7, Appli
SUMMARIES		ΙD	US-09-811-367B-3	US-09-811-367B-5	US-10-207-655-196	US-09-811-367B-1	US-10-179-528-4	US-09-919-039-130	US-10-335-009-10	US-09-284-320-86	US-10-207-655-182	US-10-179-528-3	US-10-379-127-26	US-10-451-843-1	US-10-072-012-158	US-10-072-012-160	US-10-179-528-7
		DB	6	σ	14	σ	14	10	15	10	14	14	15	16	12	12	14
		Query Match Length DB	188	188	189	189	257	179	179	199	199	199	199	231	546	549	199
	æ	Query Match	100.0	81.4	55.2	53.3	17.7	17.3	17.3	16.9	16.9	16.9	16.9	16.7	16.5	16.5	16.3
		Score	1029	838	568.5	548.5	182	178.5	178.5	173.5	173.5	173.5	173.5	171.5	170	170	168
		Result No.		7	m	4	2	9	7	80	σι	10	11	12	13	14	15

Sequence 470, App	ò	309,	309,	94	Sequence 25, Appl			8				Sequence 307, App		310,		22,	98,	98	88,	88		4, A	90,	Sequence 305, App	Sequence 487, App	Sequence 487, App		Sequence 4, Appli	Sequence 238, App
9 US-09-764-870-470		9 US-09-764-870-309			15 US-10-379-127-25	15 US-10-335-009-2		₽	14 US-10-125-540-300	13 US-10-114-893-22	P	4	15 US-10-161-493-20						10 US-09-759-130B-88				15 US-10-138-588-90	12 US-09-918-715-305	9 US-09-764-870-487		US	15 US-10-335-009-4	12 US-09-918-715-238
198						191			251	181	265	265	275	182									319	1479	189	189	399	132	1479
16.2	16.2	16.2	16.2	16.2	16.0	15.9	15.9	15.8	15.8	15.6	15.6	15.6	15.6	15.2	15.2	15.2	15.0	15.0	15.0	15.0	15.0	14.9	14.8	14.8	14.8	14.8	14.7	14.7	14.5
166.5	166.5		166.5	166.5	164.5	163.5	163.5	162.5	162.5	160.5	160.5	160.5	160.5	156	156	156	154	154	154	154	154	153	152.5	152.5	152	152	151.5	151	149.5
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	3.7	38	66	40	41	42	43	44	45

ALIGNMENTS

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Sequence 3, Application US/09811367B;
Patent No. US20020155110A1
GENERAL INFORMATION:
APPLICANT: GENINI SCIENCE, INC.
APPLICANT: Hachashi, No. US20020155110Aluaki
APPLICANT: Hachashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAPA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE.
FILE REFERENCE: 202266/0278719
CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LEGEYLGQDFYWIGLRNIDGWRWEGGPALSLRIITNSLIQRCGAIHRNGLQASSCEVALQ 180
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                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mus musculus
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Best Local Similarity
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Sequence 1, Application US/09811367B
Fatent No. US20020155110A1
GENERAL INCORMATION:
APPLICANT: GENERAL SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
FILE REPERENCE: 021286/0278119
CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
FRIOR PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
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                                                                                  61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNGGVK 120
                                                                                                             61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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                         1 MIDSVIXSMLELPTATQAQNDYGPQQKSSSSRPSCSCLVAIALGLLTAVLLSVLLYQWIL 60
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1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.3%; Score 548.5; DB 9
55.6%; Pred. No. 7.5e-50;
live 26; Mismatches 56
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Publication No. US20030166136A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
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Best Local Similarity 55.6
Matches 104; Conservative
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US-09-811-367B-1
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APPLICANT: GEMINI SCIENCE, INC.

APPLICANT: GEMINI SCIENCE, INC.

APPLICANT: TARABABAIL, No. US202020155110Aluaki

APPLICANT: TARABABAIL, No. US202020155110Aluaki

APPLICANT: TARABABAIL, No. US202020155110Aluaki

TITLE OF INVENTION: PARRACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM

TITLE OF INVENTION: PARRACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM

CURRENT APPLICATION NUMBER: US/09/811,367B

PRIOR APPLICATION NUMBER: 60/190,716

PRIOR APPLICATION NUMBER: 60/190,716

PRIOR APPLICATION UNDER: 60/190,716

PROBLEM OF SEQ ID NOS: 20

NUMBER OF SEQ ID NOS: 20
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APPLICANT: Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-INM-UNDGLOBULIN FUSION PROTEINS
FILE REPERBNCE: 39006-4.401C1
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 42.6
SOFTWARE: Patentin version 3.0
SEQ ID NO 196
LENGTH: 189
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S5.2%; Score 568.5; DB 14; Length 189;
Best Local Similarity 57.2%; Pred. No. 5.7e-52;
Matches 107; Conservative 25; Mismatches 54; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.4%; Score 838; DB 9;
80.7%; Pred. No. 1.4e-80;
tive 15; Mismatches 21
                                                                                                                                                             Sequence 5, Application US/09811367B
Patent No. US20020155110A1
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Publication No. US20030118592A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Rattus norvegicus
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Best Local Similarity 80.74
Matches 151; Conservative
                                      181 WICKKVLY 188
      181 WICKKVLY 188
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US-10-207-655-196
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US-09-811-367B-5
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FNGTH: 188
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Gaps

31;

Indels

Length 179;

141

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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kato, Seishi et al.
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAS TITLE OF INVENTION: ENCODING THESE PROTEINS
FILLE REFERENCE: GIN-6705CPUS
CURRENT APPLICATION NUMBER: US/09/284,320
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: UP 8-301429
PRIOR APPLICATION NUMBER: PCT/JP97/04056
PRIOR FILING DATE: 1996-11-13
PRIOR FILING DATE: 1997-11-07
                                                                                                                                                             --KDSTCSHCPSCPILWTRNGS 84
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                                                                                                                                                                                                      14 GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCOEKWVGYRC
                                                                                                                                                                                                                                              85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Boles, Rent S.

TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
CURRENT APPLICATION: UNBER: US/10/335,009
CURRENT FILING DATE: 2002-12-31
PRIOR PULLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 10
LENGTH: 179
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; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130
                                                                      ; Score 178.5; DB 10;
; Pred. No. 1.3e-10;
17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.3%; Score 178.5; DB 15
Best Local Similarity 31.8%; Pred. No. 1.3e-10;
Matches 54; Conservative 17; Mismatches 68
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Publication No. US20030092175A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-335-009-10
Sequence 10, Application US/10335009
Publication No. US20040001804A1
GENERAL INFORMATION:
APPLICANT: POTUNELION , Mathew A.
APPLICANT: Boles, Kent S.
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                                                                           17.3%;
31.8%;
                                                                                                                      54; Conservative
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                                                                      Query Match
Best Local Similarity
Matches 54; Conserv
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Publication No. US20030108871A1
GENERAL INFORMATION:
APPLICANT: KASST, MALTHEW R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: 05/220,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 130
LENTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 YFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGODFYWIGLRNIDG---WRWE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 RPHLSRFAMVALG----LLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 DGSA----FTINRPUFELRGGGRCAYLNGDGISSALCHSEKFWVCSR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 GGPALSLRILINSLI-----ORCGAIHRNGLQASSCEVALOWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,528
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; Score 182; DB 14;
28.7%; Pred. No. 8.3e-11;
tive 25; Mismatches 72;
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,523
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0281 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: GenBank
CLONE: 505325
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Conservative
                         CITY: Palo Alto
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                                             STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
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Best Local Similarity
Matches 48; Conserva
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NAME/KEY: misc feature

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                                                                                                                                                                                                                                                                  52 SL--LMYQRILCCGSKDSTC---SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKECADK 106
                                                                                                                                                                                                                                                                                                57 ALIALSVGQYNCPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEH 116
                                                                                                                                                                                                                                                                                                                                  107 GSHLLIFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGGPALSLRI-LINSLIQRCG 163
                                                                                                                                                                                                                                                                                                                                                       SL--LMYQRILCCGSKDSTC---SHCPSCPILMTRNGSHCYYFSMEKKDWNSSLKFCADK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 ALIALSVGQYNCPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 GSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGGPALSLRI-LTNSLIQRCG 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 NSSLH-----PESGQENDAT-----SPHFSTRHEGSFQVPVLCAVMNVVFITILII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 182, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILL REPERENCE: 330069,401C1
                                                                                                                                                                           35;
                                                                                                                                          Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 199;
                                                                                                                                                                        83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.9%; Score 173.5; DB 14;
23.8%; Pred. No. 4.8e-10;
tive 36; Mismatches 83; I
                                                                                                                                         DB 10;
                                                                                                                                   ; Score 173.5; DB 1.; Pred. No. 4.8e-10; 36; Mismatches 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
                                                                                                                                                                                                                                                                                                                                                                                                    164 AIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                   175 FLKNTEVSSMECEKNLYWICHK 196
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                                                                                                                                   ch 16.9%;
1 Similarity 23.8%;
48; Conservative 3
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NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.0
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                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-10-207-655-182
                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
Matches 48; Conserv
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                                                                                                 US-09-284-320-86
                                                LENGTH: 199
                                  SEQ ID NO 86
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; Sequence 3, Application US/10179528 ; Publication No. US20030166136A1

RESULT 10 US-10-179-528-3

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52 SL--LMYQRILCCGSKDSTC---SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 ALIALSVGOYNCPGOYTFSMPSDSHVSSCSEDWVGYORKCYFISTVKRSWTSAQNACSEH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGGPALSLRI-LTNSLIQRCG 163
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                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,528
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
Shah, Purvi
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%; Score 173.5; DB : 23.8%; Pred. No. 4.8e-10
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT UNPORMATION:
NAME: Bilings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: 291898
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Porter Drive CITY: Palo Alto
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APPLICANT: Entage, Peter C.R.
APPLICANT: Drmanac, Radoje
APPLICANT: Goodrich, Ryle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 199 amino acids
                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 23.8 Matches 48; Conservative
                                                                                                                                                                USA
                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-10-379-127-26
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79 WTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYWIGL--R
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NUMBER OF SEQ ID NOS: 1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/072,012 CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/265,514
PRIOR PILLING DATE: 2001-01-31
PRIOR PILLING DATE: 2001-01-31
PRIOR PILLING DATE: 2001-01-31
PRIOR FILLING DATE: 2001-01-31
PRIOR PILLING DATE: 2001-01-31
PRIOR PILLING DATE: 2001-01-31
PRIOR PILLING DATE: 2001-01-31
PRIOR PILLING DATE: 2001-02-02
PRIOR PILLING DATE: 2001-02-02
PRIOR PILLING DATE: 2001-02-05
PRIOR PILLING DATE: 2001-02-05
PRIOR PILLING DATE: 2001-02-05
PRIOR PILLING DATE: 2001-02-05
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PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                    Application US/10072012
5. US20040033493A1
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Anderson, David W.
Rastelli, Luca
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Lepley, Denise M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller, Charles E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colman, Steven D.
                                                                                                                                                                                                                                                                                                                      Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Furtak, Katarzyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolenc, Adam R.
Pena, Carol E. A
                                                                                                                                                                                                                                              APPLICANT: Tchernev, Velizar
                                                                                                                                                                                                                                                                           Spytek, Kimberly
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                                                                                                                                                                                                                                                                                                  Zerhusen, Bryan
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Gangolli, Esha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 21402-258
                                                222 SSVFKWICQ 230
  176 EVALQWICK 184
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Matches 39; Conserv
                                                                                                                                                                            Sequence 158, Ap
Publication No.
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APPLICANT:
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Publication No. US20040115738A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITA DI GENOVA
TITLE OF INVENTION: POLYPEptides having a triggering NK receptor activity and biologi
TITLE OF INVENTION: applications
FILE REFERENCE: 1249NKP80
CURRENT APPLICATION NUMBER: US/10/451,843
CURRENT PILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TAR

TITLE OF INVENTION: OF CELLS THAT EXPRESS DCAL-HY POLYPEPTIDES

FILE REFERENCE: NUVO-01CIP

CURRENT APPLICATION NUMBER: US/10/379,127

CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 99/799,451

PRIOR APPLICATION NUMBER: US 99/799,451

PRIOR PILING DATE: 2001-05

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.1

SEQ ID NO 26

LENGTH: 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 RSADQTVLCQSEWLKYQGKCYWFSNEWKSWSDSYVYCLERKSHLLIHDQLEMAFIQKNL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 -----CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGBYL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 GQ-DFYWIGLRNID---GWRWEGGPALSLRIL-----TINSLIQRCGAIHRNGLQASSC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 RQLNYVWIGLNFTSLKMTWTWVDGSPIDSKIFFIKGPAKENS----CAAIKESKIFSETC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SL--LMYQRILCCGSXDSTC---SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ALIALSVGQYNCPGQYIFSMPSDSHVSSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 GSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGGPALSLRI-LTNSLIQRCG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----FAMVALGLITVILM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSR----
                                                                                                                                                                                                                                                                                                                                                                                                 16.9%; Score 173.5; DB 1
23.8%; Pred. No. 4.8e-10;
iive 36; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 GLLTVILMSLLMYQRILCCG----SKDSTCSH-
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Best Local Similarity 24.9
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     JS-10-379-127-26
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US-10-451-843-1
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                                                                                      420 WKFNGGSLYYFSSVKKSWHEAEQFCVSQGAHLASVASKEEQAFLVEFTSKVYYWIGLTDR 479
                                                                                                                                                                  ---LQAS----SC 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 FAMVALGLITVILMSIL------MYORILCCGSKDSTCSHCPSCPILMTRNGSHC 86
       30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Indels
                                                                                                                                      137 NIDG-WRWEGGPALSLRILINSLIORCGA-----IHRNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NOMBER: 24-Jun-2002
CLASSIFICATION: <understandar Chicago CLASSIFICATION: <understandar Chicago CLASSIFICATION: <understandar Chicago CLASSIFICATION: <understandar Chicago CLASSIFICATION: <understandar Chicago CLASSIFICATION: <understandar Chicago CLASSIFICATION: <understandar Chicago CLASSIFICATION: <ul>
CLASSIFICATION: 
CURRENT CANADOM

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TITLE OF INVENTION: NOVBL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: «UDKNOWN»

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0281 US
  Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: 584907
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10179528
Publication No. US20030166136A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
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                                                                                                                                                                                                                                                                            533 DTPYOWVCKK 542
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Matches 39; Conserv
  39;
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                     --LQAS----SC 175
                                                    477 GIEGSWRWTDGIPF-----NAAQNKGFWEKNQSDNWRHKNGQTEDCVQIQQKWNDMTC 529
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SPOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 160
LENGTH: 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 170; DB 12;
Pred. No. 3.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
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PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
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PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
              137 NIDG-WRWEGGPALSLRILTNSLIQRCGA--
                                                                                                                                                                                                                                                             Sequence 160, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taupier Jr, Raymond J. Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
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Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                        Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colman, Steven D.
Wolenc, Adam R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carol E. A
                                                                                                                                                                                                                                                                                                                                     Tchernev, Velizar
                                                                                                                                                                                                                                                                                                                                                                                     Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Luca
                                                                                                    176 EVALQWICKK 185
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rastelli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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APPLICANT:
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Search completed: August 10, 2004, 16:32:37 Job time: 41.2619 secs

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August 10, 2004, 16:13:57; Search time 14.6407 Seconds (without alignments) 662.924 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                      sw model
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Gapop 10.0 , Gapext 0.5
                                                                    using
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1029
                                                                    protein search,
                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                        Scoring table:
                                                                    OM protein
                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                         Run on:
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	1	Appli	Appli	Appli	Appli	Appl	Appli		Appli	Appli	Appli	Appli	Appli	Appli		Appli			Appli	3, Appl	.4, Appl	Appli	Appli	Appli	Appli	Appli	Appli	•
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	Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	ID	US-08-722-126A-5	PCT-US95-04258-5	IS-08-722-126A-6	PCT-US95-04258-6	US-09-531-056A-23	US-08-690-095-9	18-08-650-578-2	US-08-688-342-3	US-09-113-788-3	US-09-113-789-9	PCT-US93-10418-2	PCT-US93-10418-4	US-08-738-462-2	PCT-US94-07587-2	US-09-531-056A-6	9-560-069-80-SN	IS-09-113-789-6	US-08-543-246B-6	US-08-543-246B-23	US-09-127-946-14	US-09-111-470-4	US-08-840-062-2	US-08-722-126A-9	PCT-US95-04258-9	US-08-690-095-7	US-09-113-789-7	US-08-543-246B-16
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	Length	188	188	114	114	16	179	179	179	179	179	199	199	225	225	191	231	231	231	231	190	316	1479	122	122	215	215	215
% Query	Match Length	81.4	81.4	53.5	m m	25.9	17.3	17.3	17.3	17.3	17.3	16.9	16.3	16.0	16.0	15.9	15.6	15.6	15.6	15.6	15.0	14.9		14.8	14.8	14.8	14.8	14.8
ć	Score	838	838	551	551	267	178.5	178.5	178.5	178.5	178.5	173.5	168	164.5	164.5	163.5	160.5	160.5	9	160.5	154	+-1	٠	152	S	152	152	152
Result	NO.	н	7	m	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Score 838; DB 3; Length 188; Pred. No. 1.8e-86;

81.4%; 80.7%;

Query Match Best Local Similarity

22,	2,2	97, Appli	8, 13,	4,4	10,	4, Appli	19,	6	24, Appl
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-08-543-246B-22 US-08-690-095-8	US-08-543-246B-2 US-08-543-246B-2	US-08-840-062-7 US-08-722-126A-8	PCT-US95-04258-8 US-09-531-056A-13	US-09-517-605-2 US-09-531-056A-2	US-09-111-470-10	US-08-688-342-4 US-09-113-788-4	US-08-543-246B-19 US-09-531-056A-4	US-08-543-246B-9	US-08-543-246B-24
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215 233	233	1487 115	115	404	273	292 292	135	216	216
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152	151	151 150.5	150.5 150	149	147.5	147.5	146 145	144	144
20.0	333	33 4	35 36	37	36	4 4	4 4 3 8	44	45

ALIGNMENTS

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Sequence 5, Application US/0872126A
Sequence 5, Application US/0872126A
Sequence 5, Application US/0872126A
Sequence 5, Application US/0872126A
Sequence 5, Application US/0872126A
Sequence 6, Application
APPLICANT: PECHT, Israel
APPLICANT: TAL Michael
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (WAFA)
MUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: ROWDY AND NEIMARK, P.L.L.C.
STATE: 0.C.
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121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG
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                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PEGHT, Israel
APPLICANT: GUTHAMNN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAPA)
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAPA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.C. : UNITED STATES OF AMERICA
                                                                                                                                                                                                                                      Sequence 6, Application US/08722126A Patent No. 6034227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: SEGULY, ROGER L. REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: PER TELECOMMUNICATION: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 628-515
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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                                                                                        181 WICKKVL 187
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                                                                                                                                   61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
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                                               1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL 60
                                                                          1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLITVILMSLLLYQRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 2004
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY AGBNT INPORMATION:
NAME: MROMET INCREATION:
    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PECHT=1 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE
TITLE OF INVENTION: FUNCTION-ASSON
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 188 amino acids
amino acid
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Best Local Similarity 80.74
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, Roger L. REGISTRATION NUMBER: 2
    151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                          181 WICKKVL 187
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PCT-US95-04258-5
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      Matches
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73 PSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYW 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                  1 PSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHILVITDNQEMSLLQVFLSEAFCW 60
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                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 179;
        DB 4; Length 76;
                                                Indels
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                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08690095

Patent No. 5792648

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.3%; Score 178.5; DB 1; Best Local Similarity 31.8%; Pred. No. 3.5e-12; Matches 54; Conservative 17; Mismatches 68;
      25.9%; Score 267; DB 4;
59.5%; Pred. No. 1.2e-22;
tive 10; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0110 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GLLTVILMSLLMYORILCCGS
                                                                                                                                                                            133 IGLRNIDGWRWEGG 146
Query Match
Best Local Similarity 59.5%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    |||||| ||: ||||| || IGLRNMSGWRWEDG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank
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LIBRARY: Gene.
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                                                                                                                                                                                                                                                                                                       US-08-690-095-9
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Patent No. 6455683
GENERAL INFORMATION:
APPLICANT: Bristol-Wyers Squibb Company
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
TITLE OF INVENTION: DNO NOTE TO SUCH APPLICATION HUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Version 3.0
SEQ ID NO 23
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 LRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 114;
                                                                  A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
FILING DATE: 08-APR-1994
ATTORNEY/AGET INPORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.5%; Score 551; DB 5; 84.1%; Pred. No. 2e-54;
                                                                                                                                               ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25,618
FP: PECHT=1 PCT
                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 6, Application PC/TUS9504258 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REPREBNCE/DOCKET NUMBER: PECH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 248633
INFORMATION FOR SEQ ID NO: 6
SEGUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
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                                                               TITLE OF INVENTION: A I
TITLE OF INVENTION: FUN
NUMBER OF SEQUENCES: 1(
CORRESPONDENCE ADDRESS:
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                               STATE: D. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-04258-6
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 RWEGGPALSLRILIN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.3%; Score 178.5; DB 2; Length Best Local Similarity 31.8%; Pred. No. 3.5e-12; Matches 54; Conservative 17; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                                                                                                                             CORRACTING SYSTEM: DOS SOFTWARE: TENTUGUEALINE SOFTWARE: TENTUGATION DATA: CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/688,342 FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0095-1 CIP TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 415-845-4166 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 179 amino acids STRANDEDNESS: single
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 GLLTVILMSLLMYQRILCCGS---
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                                                                                                                                                                                    MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: GenBank
CLONE: 1098616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-688-342-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 NCYFISSEOKTWNESRHLCASOKSSLLOLONTDELDFMSS--SOOFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KDSTCSHCPSCPILWTRNGS 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.3%; Score 178.5; DB 2; Length 179; 31.8%; Pred. No. 3.5e-12; tive 17; Mismatches 68; Indels 31
                                                                                                                  GENERAL INFORMATION:
APPLICANT: Chang, Chiwen
APPLICANT: Aramburu Beltran, Jose
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Phillips Jr., Joseph H.
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,578
                                                                                                                                                                                                                                                                                                                                                     DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ching, Edwin P.
REGIGTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0391
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415-496-1200
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,339
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5871964
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                   STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                      sequence 2, Application US/08650578
Patent No. 5811284
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-650-578-2
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                                                        US-08-650-578-2
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLFFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 LWENGSALSOYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                          17.3%; Score 178.5; DB 3;
31.8%; Pred. No. 3.5e-12;
tive 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
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GENERAL INFORMATION:
APPLICANT: Ziegler, Steven F.
APPLICANT: Hjerrild, Kathryn A.
TITLE OF INVENTION: Activation Antigen CD69
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                 ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION VUMBER: 36,749
REFERRICE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
TELERHONE: 415-855-0555
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Vicurrent Application Data:
APPLICATION NUMBER: PCT/US93/10418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 2610-WO TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 GLLTVILMSLLMYQRILCCGS-
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.8%
Matches 54; Conservative
                                                                                                                                                                                                                 179 amino acids
                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 51 Universi
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: six
                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBank
CLONE: 1098617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-10418-2
                                                                                                                                                                                                                                                                                                                                                                                     US-09-113-789-9
                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GTLGIICLSLMATLGIILKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Au-Young, Janice

APPLICANT: Goli, Surya K.

ITTLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

STRY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.3%; Score 178.5; DB 2 Best Local Similarity 31.8%; Pred. No. 3.5e-12; Matches 54; Conservative 17; Mismatches 68
                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRALION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMOUNICATION INFORMATION:
TELEFRAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ Version 1.5
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-113-789-9; Sequence 9, Application US/09113789; Patent No. 6034219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: GenBank
CLONE: 1098616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u.s.
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ZIP: 94304
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97 YFFSTTTKSWALAQRSCSEDAATLAVIDSEKDMTFLKRYSGELEHWIGLKNEANQTWKWA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 -LTVILMSLLMYQRILCCG----SKDSTCSH--CPSCPILWTRNGSHCYYFSMEKKDWN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDQQAİYABINLPIDSGPESSSPSSLPRDVCQGSPWHQFAL----KLSCAGIILLVLVVVT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                           APPLICANT: Chang, Chiwen
APPLICANT: Chang, Chiwen
APPLICANT: Lanier, Lewis L.
APPLICANT: Phillips Jr., Joseph H.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                             157 NGKEFNSWFNLTGS--GRCVSVNHKNVTAVDCBANFHWVCSK 196
                                             145 GGPAL-SLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 --LRILTNSLIQRÇGALHRNGLQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 NDLEIRGDAKENSCISISQTSVYSEYCSTEIRWICQKEL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 164.5; DB 2
Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
16.0%; Score 164.5;
Best Local Similarity 27.4%; Pred. No. 1.8e
Actches 60; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,435
FILING DATE: 16-ULL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                Sequence 2, Application US/08738462
Patent No. 5965401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPEAK: 415-496-1200
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 225 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-738-462-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C
                                                                                                                                                          RESULT 13
US-08-738-462-2
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                                                                                                                                                                                                                                       52 SL--LMYQRILCGGSKDSTC---SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADK 106
                                                                                                                                                                                                                                                                       57 ALIALSVGQYNCPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEH 116
                                                                                                                                                                                                                                                                                                                           107 GSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGGPALSLRI-LTNSLIQRCG 163
                                                                                                                                                                                                                                                                                                                                                      87 YYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRN--IDGWRWE 144
                                                                                                                                                                                                99
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                                                                                                                                                                                            11 NSSLH-----PESGQENDAT-----SPHFSTRHEGSFQVPVLCAVMNVVFITILII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 FAMVALGLLTVILMSI.L------MYQRILCCGSKDSTCSHCPSCPILWTRNGSHC
                                                                                                            Gaps
                                                                                                          35;
                                                               Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.3%; Score 168; DB 5; Length 199; Best Local Similarity 24.1%; Pred. No. 6.2e-11; Matches 39; Conservative 34; Mismatches 67; Indels
                                                                                                            83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10418
                                                             DB 5;
                                                          16.9%; Score 173.5; DB 5
23.8%; Pred. No. 1.5e-11;
tive 36; Mismatches 83
                                                                                                                                                   3 DSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application PC/TUS9310418
GENERAL INFORMATION:
APPLICANT: Ziegler. Steven F.
APPLICANT: Hierrild, Kathryn A.
TITLE OF INVENTION: Activation Antigen CD69
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2610-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             164 AIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 FLKNTEVSSMECEKNLYWICNK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 199 amino acids
amino acid
                                                                                                          48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein PCT-US93-10418-4
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
  ;
PCT-US93-10418-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Sea
STATE: Wa
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US93-10418-4
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                                                               Query Match
                                                                                                        Matches
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ð g ð --AGECAYLND 168

Gaps

49;

Length 191; Indels

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57 SAIRANCHQEPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESF 116
                                                                                                                                                                                                                                                                                                       64 -SKDSTCSHCPS-----CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDN 116
                                                                                                                                                                                                                                                                                                                                                                                          ----PALSLRILTNSLIQRCGAIHR 167
                                                                                                                                                                                                                                           11 ELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVI--LMSLLMYQRILCCG----
                                                                                                                                                                                                                                                                                                                                                                                                                                   117 ÓBLNFLLRYKGPSDHWIGLSREQGOPWKWINGTEWTROFFILG--
                                                                                                                             15.9%; Score 163.5; DB 4; 25.3%; Pred. No. 1.9e-10; tive 21; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                          117 QGVKLFGEYLGQDFYWIGLRNIDG--WRWEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: August 10, 2004, 16:20:31 Job time : 14.6407 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 NGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 KGASSARHYTERKWICSK 186
                                                                                                                                                                                                                                                           15 ELPANPGCLHSKEHSIKA
                                                                                                                             Query Match
Best Local Similarity 25.39
Matches 50; Conservative
SEQ ID NO 6
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                       US-09-531-056A-6
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APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: DB20 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLKFCADKGSHLLTFPDDVQGVKLFGEYLGQD---FYWIGLR---NIDGWRWEGGPALS- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MADSSIYSTLELP--EAPQ-----VQDESRWKLKAVLHRPHLSRFAMVALGL--- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDQQAIYAELNLPTDSGPESSSPSSLPRDVCQGSPWHQFAL----KLSCAGIILLVLVVT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 -LTVILMSLLMYQRILCCG----SKDSTCSH--CPSCPILWTRNGSHCYYFSMEKKDWN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.0%; Score 164.5; DB 5; Length 225; 27.4%; Pred. No. 1.8e-10; tive 32; Mismatches 90; Indels 37
                                                                                                           PURÎFIED MAMMALIAN NK ANTIGENS AND
RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 NDLEIRGDAKENSCISISQTSVYSEYCSTEIRWICQKEL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 -- LRILTNSLIQRCGAIHRNGLQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                   ZIP: 07940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Ward 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: DX0397K
TELEPHONE: 201-822-7055
TELEPHONE: 201-822-7039
                                        Sequence 2, Application PC/TUS9407587
GENERAL INFORMATION:
APPLICANT: Schering Corp.
TITLE OF INVENTION: RELATED MAMM
TITLE OF INVENTION: RELATED REAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09531056A
Patent No. 6455683
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                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESONDENCE ADDRESS:
ADDRESSEE: Schering Corp.
STREET: One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 27.4
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein PCT-US94-07587-2
                                                                                                                                                                                                                                                             New Jersey
USA
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CITY: Madison
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US-09-531-056A-6
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                          PCT-US94-07587-2
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model - protein search, OM protein

Run on:

(without alignments) 1509.673 Million cell updates/sec August 10, 2004, 16:12:27; Search time 11.9788 Seconds

US-09-811-367B-5 Title: Perfect

1036 1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188 score: Seguence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cell functi	lymphocyte early a	gene 17.5 protein	natural killer cel	hNKR-Pla protein -	Ä	lectin	natural killer cel	NKR-P1 protein hom	NK-cell_receptor P	asialoglycoprotein	C type lectin, B l	phospholipase-A(2)	natural killer cel	.ycoprc	lectin, galactose/	HIV gp120-binding	scavenger receptor	lectin M-ASGP-BP p	type II lectin-lik	agkisacutacin beta	natural killer cel	B-cell surface ant	secretory phosphol	secretory phosphol	asialoglycoprotein	natural killer cel		hepatic lectin hom
SUMMARIES	ID	I59421	JH0822	I50146	A46467	138700	B46467	LINRT2	T28140	C46467	A35917	S13165	T28141	S48719	PT0375	S29855	JX0209	A46274	JC7595	A42230	JC7608	JC7135	PT0372	A43532	B56395	A56395	LINHUZA	I54524	LNRTL	WMVZF2
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	* Query Match	100.0	17.8	17.8	16.7	16.4	16.1	16.0	15.7	15.4	15.4	15.4	15.3	15.3	15.2	15.1	14.9	14.8	14.8	14.3	14.3	14.1	13.8	13.8	13.7	13.7	13.6	13.4	13.4	13.2
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hepatic lectin – c natural killer cel	aggretin alpha cha	mannose receptor,	hepatic lectin H1	versican precursor	phospholipase A2 r	IGE Fc receptor, 1	Kupffer cell recep	versican precursor	versican precursor	Ly-49G.2 antigen -	versican precursor	IgE Fc receptor II	coagulation factor	receptor DEC-205 -
LNCHL PT0374	PC7027	T42710	LNHU1	A55535	A49707	LINMSER	A28166	T14274	T42389	I49053	A60979	S34198	JC4691	S58880
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13.2	13.0	13.0	12.9	12.9	12.8	12.6	12.6	12.6	12.6	12.6	12.5	12.4	12.3	12.3
136.5	134.5	134.5	134	134	132.5	131	131	131	131	130.5	130	128	127.5	127.5
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associated antigen - rat

mask cell indiction associated antigen - rat C.Species: Rattus norvegicus (Novay rat) C.Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 05-Nov-1999

Riguthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A;Reference number: I59421; MUID:96016176; PMID:7568140
A;Accession: I59421

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-188 <RES>
A;Crossreferences: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C;Genetics: A;Genetics:
ö Gaps .; 0 Length 188; Indels 100.0%; Score 1036; DB 2; ilarity 100.0%; Pred. No. 3.2e-90; Conservative 0; Mismatches 0; Local Similarity les 188; Conserv Query Match Best Loca Matches

9 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL ď

09 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLITVILMSLLLYQRTL g

CCGSKGFMCSOCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120 61 CCGSKGFMCSQCSRCPNLMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120 61 à g 121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180 121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180 qq à

WICEKVLP 188 181 WICEKULP 188 181 qq à

lymphocyte early activation antigen AIM/CD69 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Josep-1993 #sequence revision 20-Aug-1994 #text_change 08-Oct-1999 C;Accession: JH0822; I56167; S60753 R;Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M.; Exp. Med. 178, 537-547, 1993 A;Title: Molecular cloning, expression, and chromosomal localization of the human earli mitting receptors.
A;Reference number: JH0822; MUID:93340630; PMID:8340758

A; Molecule type: mRNA A;Accession: JH0822

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NAIternate names: NKR-PI protein
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
C;Accession: A46467; A46502; A46456
R;Giorda, R.; Trucco, M.
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: A46467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A MOJECULE LYPE: MRNA
A; Residues: 'MHLLCT',1-27 <GIO>
A; Residues: 'MHLLCT',1-27 <GIO>
A; Residues: 'MHLLCT',1-27 <GIO>
A; Cross-references: GB:MY7676; NID: g200058
A; Experimental source: A-LAK cells, C57BL
A; Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence
R; Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.
J. Immunol. 149, 1957-1963, 1992
A; Title: Genomic structure and strain-specific expression of the natural killer cell re
A; Reference number: A46502; MUID:92388663; PMID:1517565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-109,'H',111-181,'D',183-227 <GI2>
A;Cross-references: GB:X64716; NID:g53395; PIDN:CAA45971.1; PID:g817989
A;Experimental source: BALB/c 3T3 fibroblastoid cell line
A;Mote: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113072
B;Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
J. Immunol. 147, 3229-3236, 1991
A;Title: cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of A;Reference number: A46456; MUID:92013158; PMID:1680927
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                                                                         101 PC----MLVLALVAVIVL----QRPSCSPRPPF----SHVCFNAWVGFQGKCYYFSDT 146
                                                                                                                                                                                                           147 ESDWNSSREHCHRLGASLATLDTKEEMEFMLQYQRPADRWIGLHRAEGDEHWTWADGSAF 206
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          PCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSME
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A,Residues: 1-38, L',40-227 <YOK>
A,Residues: 1-38, L',40-227 <YOK>
A,Cross-references: GB:M7753; NID:g198569; PIDN:AAA39366.1; PID:g198570
A,Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                       207 T----NRPVFELRGGGRCAYINGDGISSALCHSEKFWVCSR 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 natural killer cell receptor P1 - mouse
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Matches 53; Conservative
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A.Accession: S60753
A.Accession: S60753
A.Accession: S60753
A.Accession: S60753
A.Accession: S60753
A.Accession: DNA
A.Accession: DNA
A.Accession: 1-199 < SAN>
A.Residues: 1-199 < SAN>
A.CCOSS-references: EMBL:Z30426; NID:g525242; PIDN:CAA83017.1; PID:g558352
C.Comment: This protein is the earliest inducible cell surface glycoprotein expressed in
A;Cross-references: GB:Z22576; NID:g397938; PIDN:CAA80298.1; PID:g397939
A;Note: the authors translated the codon CAA for residue 110 as GLu
B;Hamann, J.; Fiebig, H.; Strauss, M.
J. Immunol. 150, 4920-4927, 1993
A;Title: Expression cloning of the early activation antigen CD69, a type II integral mem
A;Reference number: I56167; MUID:93267093; PMID:8496594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;18,30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted F;166/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 39, 221-229, 1994, Affile: Inkeptics 39, 221-229, 1994, Affile: Linkage of a new member of the lectin supergene family to the chicken Mhc genes A; Reference number: 150146; MUID:94164691; PMID:8119728 A, Accession: 150146
                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1; PID:g291898
R;Santis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
Eur. J. Immunol. 24, 1692-1697, 1994
A;Title: Structure of the gene coding for the human early lymphocyte activation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG--WRWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 VKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVGLKKEPGHPWKWSNGKEF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene 17.5 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 VSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMC---SQCSRCPNLWMRNGSHCYYFSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:CD69
A;Cross-references: GDB:132925; OMIM:107273
A;Map position: 12p13-12p12
C;Superfamily: C-type lectin homology
C;Superfamily: C-type lectin homology
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;39-64/Domain: C-type lectin homology sLGHs
F;38-194/Domain: C-type lectin homology sLGHs
F;18-194/Domain: C-type lectin homology sLGHs
F;18-194/Domain: C-type lectin homology sLGHs
F;18-10/Binding site: phosphate (Firs) (covalent) (by protein kinase C) #st
F;31/Binding site: phosphate (Inr) (covalent) (by casein kinase II) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Cross-references: GB:M88072; NID:g505324; PIDN:AAA48558.1; PID:g505325
C;Superfamily: C-type lectin homology
F;129-241/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.8%; Score 184; DB 2; Length 257;
larity 28.6%; Pred. No. 6.8e-10;
Conservative 23; Mismatches 66; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 N-NWENVTGSDKCVFLKNTEVSSMECEKNLYWICNK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30; Mismatches
                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Bernot, A.; Zoorob, R.; Auffray, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-199 <RES>
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hepatic lectin 2 - rat
N;Alternate names: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3)
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Accession: B28462; A28462; A31601; A26888; A25417
R;Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, A J. Biol. Chem. 262, 9938, 1987
A;Title: Major and minor forms of the rat liver asialoglycoprotein receptor are independence number: A28462; MUID:87250656; PMID:3597443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-152,'A',154-201,'I',203-259,'C',261-301 <MCP>
A; Residues: 1-152,'A',154-201,'I',203-259,'C',261-301 <MCP>
A; Cross-references: GB: M16347; NID: g206648; PIDN: AAA42038.1; PID: g206649
A; Note: the authors translated the codon GCA for residue 153 as Arg and ATT for residue R; Drickamer, K:; Mamon, J.F.; Binns, G.; Leung, J.O.
J. Biol. Chem. 259, 770-778, 1984
A; Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evi. A; Reference number: A25417; MUID: 84111554; PMID: 6319386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 88-96,'X',98-118,'X',120;129-158;177-182,'X',184,'X',186-189;192-290,'C',29
R;Sanford, J.P.; Elliott, R.W.; Doyle, D.
DNA 7, 721-728, 1988
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A; Residues: 201-259, C', 261-281, 'ND', 284-301 cDRI>
C; Comment: Calcium is required for ligand binding.
C; Comment: Calcium; sequired for ligand binding.
C; Superfamily: heatic lectin; C-type lectin; liver;
C; Superfamily: heatic lectin; lectin; liver;
F; 2-60/Domain: intracellular #status predicted <INT>
F; 2-61/Domain: transmembrane #status predicted <INT>
F; 8-301/Domain: extracellular #status predicted <EXT>
F; 78-301/Domain: c-type lectin homology <ICH>
F; 97,119,165/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-301 <SAN>
A; Residues: 1-301 <SAN>
A; Cross=references: GB:X07636; NID:g57066; PIDN:CAA30476.1; PID:g57067
B; McPhaul, M.; Berg, P.
Mol. Cell. Biol. 7, 1841-1847, 1987
A; Title: Identification and characterization of cDNA clones encoding two homologous ]
A; Reference number: A26888; MUID:87257885; PMID:3600647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.
A;Reference number: A31601; MUID:89170119; PMID:3234178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 RTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 EQEFVVKHRĞAFHIMIĞLTDKDĞSWKWVDĞTEYRSNFKNWAFTQPDNWQGHEEGGSEDCA 272
                                 FCADKGSHLLTFFDNQGVNLFQEYVGEDF--YWIGLR----DIDGWRWEDGPALS---LS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 RILICQLAFFLSNGTECCPVNWVEFGGSCYWFSRDGLTWAEADQYCQMENAHLLVINSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Residues: 1-301 <HAL>
A;Cross-references: GB:J02762; NID:g205162; PIDN:AAA41522.1; PID:g205163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 165.5; DB 1;
Pred. No. 4.4e-08;
                                                                                                                                                                                         itgdtengscasisgdkvtsescstdnrwicokel 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.0%; Scor.
27.3%; Pred. No. 4...
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 39; Conserv
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B46467

NKRP 21

NKRP 21

NKRP 21

NKRP 22

NKRP 22

NKRP 22

NKRP 23

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999

C; Accession: B46467

J. Immunol. 147, 1701-1708, 1991

A; Pritle: A family of genes selectively coexpressed in adherent lymphokine-activated kill A; Accession: B46467; MUD: 91349596; PMID: 1880421

A; Accession: B4647

A; Accession: Preliminary

A; Molecule type: mRNA

A; Residues: 1-223 < GIO>

A; Cross-references: GB, NY7677; NID: 92200060; PIDN: AAA39823.1; PID: 92200061
                                                                                                                                                                                                                                                                                             the C-type lectin superfamily ex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 TVILMSLLLYQRTLCCG----SKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGED--FYWIGLR---DIDGWRWE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --AAPR-VQDDSRWKVKAVLHRPC--VSYLVMVALGLL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDQQAIYAELNLPTDSGPESSSPSSLPRDVCQGSPWH-QFALKLSCAGIILLVLVVVTG-L 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --RCPNLWMRNGSHCYYF 89
                                                                                                                       Cispeciaes: Homo sapiens (man)
Cispeciaes: Homo sapiens (man)
Cispeciaes: Homo sapiens (man)
Cispacesion: 138700

Filanier, L.i. Chang, C.; Phillips, J.H.
J. Immunol. 153, 2417-2428, 1994
A; Title: Human NRR-Pla. A disulfide-linked homodimer of the C-type lectin su A; Reference number: 138700; MUID:94358407; PMID:8077657
A; Accession: 138700
A; Reference number: 128500; MUID:94358407; PMID:8077657
A; Reference number: 128500; MUID:94358407; PMID:8077657
A; Residues: 1-225 < RES>
A; Residues: 1-225 < RES>
A; Residues: 1-225 < RES>
A; Residues: 1-225 < RES>
A; Residues: Call receptor Pi; C-type lectin homology < LCH>
F; 94-210/Domain: C-type lectin homology < LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VXADLNLARIQEPKHDSPPSLSPDTCRCPRW-----HRLALKFGCAGLILLVLVVIGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Note: sequence extracted from NCBI backbone (NCBIN:52380, NCBIP:5238:
C; Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: transmembrane protein
F;94-210/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.1%; Score 167; DB 2;
23.3%; Pred. No. 2.3e-08;
tive 34; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.4%; Score 169.5; DB 2, 26.1%; Pred. No. 1.4e-08; ive 32; Mismatches 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 TVILMSLLLYQRTLCCGSKGFMCSQCS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 IYSTLELPAAPRVQDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MADNSIYSTLELP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                        I38700
hNKR-Pla protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
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Asialoglycoprotein receptor - mouse
NiAlternate names: hepatic lection
NiAlternate names: hepatic lection
NiAlternate names: hepatic lection
CjSpecies: Mus musculus (house mouse)
CjSpecies: Mus musculus (house mouse)
CjAccession: S13165
R;Sanford, J.P.; Doyle, D.
Biochim. Biophys. Acta 1087, 259-261, 1990
A;Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor gene A;Reference number: S13165; MUID:91027942; PMID:2223888
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rigiorda, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, Science 249, 1298-1300, 1398-1308 Astribe: NRR-Pl, a signal transduction molecule on natural killer cells.

A;Reference number: A35917; MUID:90378305; PMID:2399464
                                                                                                                                                                                                                                                                                                                       75 CPNLWMRNGSHCYYFSMEXRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDF--YW 132
                                                                                                                                                                                                                                                                                                                                                                91 CPQDWLLHRDKCFHVSQVSNTWEEGQADGGRKGATLLLIQDQEELRFLLDSIKEKYNSFW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 LALVGMSILVRVLVQKPSVEPCRVLIQENLSKTGSPAKL----KCPKDWLSHRDKCFHV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVG--EDFYWIGLR---DIDGWRWE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQTSITWKESLADCGGKGATLLLVQDQEELRFLRNLTKRISSSFWIGLSYTLSDENWKWI 168
                                                                                                                                                                                                                                                38 RIALKISCAGLILLV----LTLIGMSVLVVRVLVQKPSREKCC---VFIQENLNKTTVNLE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 LVMVALGLLTVILMS-----LLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYF 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Apr-1991 #seguence_revision 12-Apr-1991 #text_change 24-Sep-1999
C;Accession: A35917
                                                                                                                                                                                                                                                                                                                                                                                                                                    133 IGLR----DIDGWRWEDGPALSLSILSNSVVQK---CGTIHRCGLHASSCEVALQWICEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723 CS:Superfamily: natural Killer cell receptor P1; C-type lectin homology C;Keywords: transmembrane protein C;Keywords: transmembrane protein P:94-210/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                          27 KAVLHRPCVSYLVMVALGLLTVILMSLLLY-----QRTLCCGSKGFMCSQCSR-
                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                              Length 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                     1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
15.4%; Score 159.5; DB 2
Best Local Similarity 23.5%; Pred. No. 1.2e-07;
Matches 39; Conservative 33; Mismatches 73
                                                                                           15.4%; Score 159.5; ilarity 25.3%; Pred. No. 1.2e Conservative 33; Mismatches
        C;Keywords: transmembrane protein F;91-207/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NK-cell receptor P1 - rat
                                                                                                                  Local Similarity
Les 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-223 <GIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A35917
A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 VL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 EL
                                                                                           Query Match
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                                                                                                                     Best Loca
Matches
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Molecule type: mSNA
A;Experimental source: NK cells, C57BL7B
A;Experimental source: NK cells, C57BL7B
A;Note: sequence extracted from NCBI backbone (NCBIN:52382, NCBIP:52383)
B;Nyan, J.C.; Turck, J.; Ntemi, E.C.; Yokoyama, W.M.; Seaman, W.B.
J. Immunol. 149, 1631-1635, 1992
A;Title: Molecular cloning of the NK1.1 antigen, a member of the NKR-P1 family of natura
A;Accession: A46499
A;Status: preliminary
                                                                                                                                                                                                                   C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28140
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility compl
A;Reference number: Z20475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: C46467; A46499
R;Giorda, R.; Trucco, M.
Li Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: C46467
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-70 <MIL>
A;Coss-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
A;Experimental source: clone cB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 CSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFPDNQGVNLFQEYVGEDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 CLLCPQFWRLLGDRCYELSTEKGNWTQAKMKCENLQSQLAVLRKKAEEDHLQQMAGAEPV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 WIGLR-DIDGWRWEDGPAL----SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N, Alternate names: natural killer cell activation molecule; NK1.1 alloantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Experimental source: C57BL/6J NK cells (NCBIN:111622, NCBIP:111624) Superfamily: natural killer cell receptor P1; C-type lectin homology
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A;Residues: 1-86,90-220 <RYA>
A;Cross-references: GB:S43141; NID:9254094; PIDN:AAB22979.1; PID:9254095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: Intron positions not resolved (incomplete sequence)
                                                                                                                                                                                               natural killer cell receptor homolog - chicken (fragment)
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ches 60;
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28.1%; Pred. No. 4.8e
ive 16; Mismatches
  164 TIHRCGL-HASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKR-P1 protein homolog gene-40 - mouse
                                   34; Conservative
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A,Map position: 16
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Best Local S:
Matches 34,
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Query Match

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A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I: A;Reference number: PT0372; MUID:91178434; PMID:2007850
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R; Takezawa, R.; Shinzawa, K.; Watanabe, Y.; Akaike, T.
Biochim. Biophys. Acta 1172, 220-222, 1939
A; Title: Determination of mouse major asialoglycoprotein receptor CDNA sequence.
A; Reference number: $29855; WUID:93176818; PMID:8439566
                                                                                                                                                                                                                                                                                                                                  CDATWORNGSSRICYQFNILSSLSWNQAHSSCLMQGGALLSIADEDEEDFIRKHLSKVVK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 IRFIIMVA--IWSAVFLNSLFNQEVQIPLTE----SYCGPCPKNWICYKNNCYQFFDESK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 CPNLWMRNGSH--CYYFS-MEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE--D 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 EVWIGLNQLDEKAGWQWSDGTPLSYLNWSQEITPGPFVEHHCGTLEVVSAAWRSRDCEST 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       natural killer cell receptor group 2-D - human N;Alternate names: integral membrane protein NKG2-D C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 05-May-2000 C;Accession: PTG375; S15611; $19110 R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 VSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-284 cTAK>
A, Cross-references: EMBL:D13517; NID:g220480; PIDN:BAA02734.1; PID:g220481
C, Superfamily: hepatic lectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: X54870; NID: 935062; PIDN: CAA38652.1; PID: 935063
                                                                                                               Length 1487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%; Score 157; DB 2; Length 216;
larity 26.4%; Pred. No. 2e-07;
Conservative 33; Mismatches 62; Indels
F;181-222/Domain: fibronectin type II repeat homology <2F1>F;380-503/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                          130 FYWIGLRDID---GWRWEDGPALSLSILSNSVVQKCGTIHRCGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: natural killer cell
A, Note: translation of nucleotide sequence is not complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SILSNSVVQKCGTIHRCGLHASS-----CEVALQWIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211
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                                                                                                                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: glycoprotein; transmembrane protein
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                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOWICEKVL 187
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LPYICKRDL 360
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                         Local Similarity
les 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PT0375
A; Molecule type: mRNA
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28141
R;Wilne, S.; Kaufman, J.; Beck, S.
B;Wilne, S.; Kaufman, J.; Beck, S.
B;Wilne, S.; Kaufman, J.; Beck, S.
B;Wilne, S.; Kaufman, Jack, S.
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O'-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C;Accession: 548719
R;Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita, H.
Bur. J. Biochem. 225, 375-382, 1994
A;Title: Structural comparison of phospholipase-A(2)-binding regions in phospholipase-A(A;Reference number: S48719; MUID:95010128; PMID:7925459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    re
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C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
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A, Experimental source: clone cB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 RTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDNQGVNLFQEYVGEDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIGLRDIDG----WRWEDGPALS--LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KCG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 BODFVVKHRSQFHIWIGLTDRDGSWKWVDGTDYRSNYRNWAFTQPDNWQGHEQGGGEDCA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAQCPFDWIGFRGKCYYFSEDESNWTSSQNNCSALGASLAVFDSAEDLSFTWRHKGSSPH 86
                                                                                                                                                                                                                                                                                                                          Gaps
                                     A;Cross-references: EMBL:X53042; NID:g53104; PIDN:CAA37211.1; PID:g53105 Cs. Superfamily: hepatic lectin; C-type lectin homology C;Keywords: glycoprotein; liver; transmembrane protein F;170-293/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                           DB 2; Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 156;
                                                                                                                                                                                                                                                                                                                          67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 GVNLFQEYVGEDFYWIGLRDIDG-WRWEDGPALSLSILSNSVVQ-
                                                                                                                                                                                                                                   15.4%; Score 159.5; DB 2; 26.6%; Pred. No. 1.6e-07; tive 23; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 15.3%; Score 158; DB 2; Similarity 27.5%; Pred. No. 1.2e-07; 33; Conservative 22; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : : |: ||||
EILSDGHWNDNFCQQVNRWVCEK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 TIHRCG-LHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                      38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 16
A;Introns: 17/1; 74/3; 110/2
                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Status: preliminary
A Molecule type: mRNA
A Residues: 1-1487 <HIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-156 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
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Best Local 9
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Matches

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F;153-276/Domain: C-type lectin homology <LCH>
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	4,	102	180	155	240			
	24; Gaps	NSSLKF	TEADKY		WRPEQP			
	24;	MEKRDW	SSVRPW	SISIE	: STGFON			
Length 284	Indels	NGSHCYYFSN	YEGSCYWFS:	WRWEDGPALS	: WKWVDGTDYE	L 187	L 280	
2;]	75;	NLWMR	INWVE	DIDG-1	DONGP!	QWICEKV	VCETK	
e 156; DB	lismatches	SQCSRCP	GNGSERTCCP	GEDFYWIGLR	GPLNTWIGLT	CEVALQW	DDVCRRPYRW	
Scor	20, 19	1	OMAAFR	LFQEYV	FLORHIM	SS	FDGRWN	
15.1%;	ive	SKGFMC	YRSLSC	DNQGVN	SRDEQN	RCGLHA	, DCAHFT'	
Query Match 15.1%; Score 156; DB 2; Length 284; Best Local Similarity 25.6%; Pred No. 3.26-07.	Matches 41; Conservative 20; Mismatches 75; Indels	52 SLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDMNSSLKF 102	121 SLLIHVKOLVSDVRSLSCOMAAFRGNGSERTCCPINWVEYEGSCYWFSSSVRPWTEADKY 180	CADKGSHLLTFP	181 CQLENAHLVVVTSRDEQNFLQRHMGPLNTWIGLTDQNGPWKWVDGTDYETGFQNWRPEQP 240	156 -NSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187	241 DNWYGHGLGGGEDCAHFTTDGRWNDDVCRRPYRWVCETKL 280	
atch	41	52	121	103	181	156	241	
Query Ma	Matches	<i>\$</i> 5	Db	δγ	pp	δy	đ	

Search completed: August 10, 2004, 16:19:36 Job time: 11.9788 secs

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GenCore version 5.1.6
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sw model using protein search, 1 protein Ö

August 10, 2004, 16:05:41; Search time 7.32035 Seconds (without alignments) 1337.256 Million cell updates/sec Run on:

1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188 US-09-811-367B-5 1036 Perfect score: Sequence: ritle:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Resu. N

	Description	Describtion	Q07108 homo sapien		P27812 mus musculu	Q9mzk9 macaca mula	P08290 rattus norv	P27814 mus musculu	P27471 rattus norv	P24721 mus musculu	Q9mzj7 macaca mula	P26718 homo sapien	homo	Q9mz41 pan troglod	mus	P14371 fowlpox vir	•	P34927 mus musculu	homo	Q95mi4 pan troglod	pan	agki	P49301 rattus norv	Q9mzj3 macaca mula	P26715 homo sapien	P21854 homo sapien		Q9gme8 pan troglod		homo	рошо		fowlpos	gallus	Q9mzk6 macaca mula
	£	TT	CD69 HUMAN	NK11 MOUSE	NK12 MOUSE	CD94 MACMU	LECI_RAT	NK14 MOUSE	NK13 RAT	LECI_MOUSE	NKGD_MACMU	NKGD HUMAN	CD94_HUMAN	CD94 PANTR	MMGL MOUSE	V239_FOWPV	CD69_MOUSE	LECH_MOUSE	CLE2 HUMAN	NKGE PANTR	NKGA_PANTR	RHCA AGKRH	MMGL RAT	NKGA_MACMU	NKGA HUMAN	CD72 HUMAN	CVXB_CRODU	NKGC PANTR	LECI HUMAN	LY75_HUMAN	NKGE HUMAN	LECH RAT	V008 FOWPV	LECH_CHICK	NKGC_MACMU
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	Query Match Length	nengen	199	227	223	179	301	220	223	301	216	216	179	179	304	163	199	283	149	240	233	133	306	233	233	359	148	233	311	1722	240	283	167	207	231
~	Query	March	17.8	16.7	16.1	15.8	15.6	15.4	15.4	15.4	15.3	15.2	15.0	15.0	14.9	14.9	14.9	14.9	14.8	14.7	14.4	14.3	14.3	13.9	13.8	13.8	13.6	13.6	13.6	13.5	13.4	13.4	13.2	13.2	13.0
	d L	2007	184.5	172.5	167	163.5	161.5	159.5	159.5	159.5	159	157	155	155	154.5	154	154	ın	153.5	2		148.5	148.5	143.5	142.5	142.5	140.5	140.5	0	139.5	139	139		136.5	134.5
	ult No		П	7	М	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	29	30	31	32	33

SEQUENCE FROM N.A.

P07306 home sapien P70194 mus musculu Q9erb4 rattus norv Q62059 mus musculu P26717 home sapien P81509 crotalus ho P49260 oryctolagus Q99999 aqfistrodon P20659 mus musculu P10716 rattus norv P81282 bos taurus	
LECH HUMAN KUCR MOUSE PGCV RAT PGCV MOUSE NKGC HUMAN CHBB CROHO PAZR RABIT MMHA AGKHA FCEZ MOUSE KUCR RAT PGCY BOVIN	MINITE AGENTA
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290 548 2738 3358 231 117 1458 157 331 550	14p
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134 133.5 132.5 132.5 132.5 131 131 131	067
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ALIGNMENTS

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MEDLINE-93340630; PubMed=8340758;
LOPEZ-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,
LOPEZ-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,
BSCH F., Sanchez-Mateos P., Sanchez-Madrid F.;
"Molecular cloning, expression, and chromosomal localization of the human earliest lymphocyte activation antigen AIM/CD69, a new member of the C-type animal lectin superfamily of signal-transmitting
                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Early activation antigen CD69 (Early T-cell activation antigen p60)
(GP32/28) (Leu-23) (MLR-3) (EAl) (BL-AC/P26) (Activation inducer molecule) (AIM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular characterization of the early activation antigen CD69: a type II membrane glycoprotein related to a family of natural killer cell activation antigens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=93314711; PubMed=8100776;
Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIME=94298875; PubMed=8026529; Sarauss M., Sanchez-Madrid lastis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid lastructure of the gene coding for the human early lymphocyte activation antigen CD69: a C-type lectin receptor evolutionarily related with the gene families of natural killer cell-specific
                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 96-103; 128-146 AND 189-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamann J., Fiebig H., Strauss M.; "Expression cloning of the early activation antigen CD69, integral membrane protein with a C-type lectin domain."; J. Immunol. 150.4920-4927(1993)
199 AA.
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PRT;
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MEDLINE=93267093; PubMed=8496594;
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STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                              92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG--WRWEDGPAL 149
                                                                                                                                                                                                                                   45 VMNVVFITILILIALIALSVGQYN---CPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFIST 101
                                                                                                                                                                                                                                                                                                  102 VKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWYGLKKEPGHPWKWSNGKEF 161
                                                                                                                                                                                                                35 VSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMC---SQCSRCPNLWMRNGSHCYYFSM 91
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giorda R., Trucco M.;
"Mouse NKR-P1. A family of genes selectively coexpressed in adherent
lymphokine-activated killer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NKR-P1 2) (NKR-P1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of a natural killer cell gene complex on mouse chromosome 6.";
                                                                                                                                               DB 1; Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92013158; PubMed=1680927;
Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M. Seaman W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - FUNCTION: May function as signal-transmitting receptor. -! - SUBMNIT: Homodimer; disulfide-linked. -! - SUBCELLULAR LOCATION: Type II membrane protein. -! - IISSUE SPECIFICITY: Natural killer cells. -! - IISSUE CONTAINS: COTAINS I C-type lectin family domain.
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                               66 N-LINKED (GLCNAC. . .) (PC
22559 MW; 172E2699D2FBBDFB CRC64;
                                                                                                                                                        4.5e-11;
                                                                                                                                                                                                                                                                                                                                             SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                        N-NWFNVTGSDKCVFLKNTEVSSMECEKNLYWICHK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Natural killer cell surface protein P1-2 (NKR
                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                              30; Mismatches
                                C-TYPE LECTIN
                                                                                                                                               17.8%; Score 184.5;
                                                                                                                                                                Pred. No.
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MEDLINE=91349596; PubMed=1880421;
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                                                                                                                                                                  26.3%;
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                 199
195
194
194
166
               62 1
92 1
68 1
96 1
173 1
166 1
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HSSP; P22897; 1EGG.
                                                                                                                                                             Local Similarity
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P27811;
                              DOMAIN
DISULFID
DISULFID
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Matches
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TISSUE SPECIFICITY: Natural killer cells.
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169
186
223 AA;
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189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 LKFCADKGSHLLTFPDNQGVNLFQEYVGEDF--YWIGLR----DIDGWRWEDGPALS--- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSS 99
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                                                                                                                                                                                                                                                                                                                 EXTRACELLUIAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giorda R., Weisberg E.P., Ip T.K., Trucco M.; "Genomic structure and strain-specific expression of the natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.7%; Score 172.5; DB 1; Length 227;
                                                                                                                         SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C TYPE_LECTIN 2; 1.
Glycoprotein; Autigen; Transmembrane; Signal-anchor; Lectin.
DOMAIN
CYTOPLASMIC (POTENTIAL).
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-1. Immunol. 149:1957-1963 [1992).
-1. FUNCTION: May function as signal-transmitting receptor.
-1. SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S -> L (IN REF. 2).
0599A2587DF0B615 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Natural killer cell surface protein Pl-34 (NKR-Pl 34).
KLRBIB OR LYSSB OR LYSS-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKITGDTENDSCAAISGDKVTFESCNSDNRWICQKEL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7.9e-10;
5; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
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MEDLINE=92388663; PubMed=1517565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. 147:1701-1708(1991).
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                                                                      Pfam; PF00059; lectin c; 1.-
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 S
25689 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Conservative
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MGD; MGI:107540; Klrbla.
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1105
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186
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CARBOHYD
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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NK12_MOUS

NK12_MOUS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMART; SMOO34; CLECT; 1.
PROSITE; PSSO0615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PSSO041; C_TYPE_LECTIN 2; 1.
Glycoprotein; Antigen; Transmedbrane; Signal-anchor; Lectin.
DOMAIN

44 CYTOPLASMIC (POTENTIAL).

45 G3 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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QWAZE3, OSGK91; OSMXK7; Q9MXK8;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
12-OCT-2003 (Rel. 42, Last annotation update)
13-OCT-2003 (Rel. 42, Last annotation update)
14-OCT-2003 (Rel. 42, Last annotation update)
15-OCT-2003 (Rel. 42, Last annotation update)
16-OCT-2003 (Rel. 42, Last annotation update)
17-OCT-2003 (Rel. 42, Last annotation update)
18-OCT-2003 (Rel. 42, Last annotation update)
18-OCT-2003 (Rel. 42, Last annotation update)
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C.TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N.LINKED (GLCNAC. . .) (POTENTIAL).
N.LINKED (GLCNAC. . .) (POTENTIAL).
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
NCBI_TaxID=9544;
[1]
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:- SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M77677, AAA39823.1; -.
EMBL, X64721; CAA45974.1; -.
PIR, B46467; B46467.
MGI:107539; Kirblb.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
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PRINTS; PR00356; ANTIFREEZEII.
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FYWIGL----RDIDGWRWEDGPALSLSILSNSVVQK---CGTIHRCG-LHASSCEVALQWI

CEKVL 187

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56 SDCCSCHEKWVGYRCNCYFISSEEKTWNESRHFCASQKSSLLQLQNRDELDFMSS--SQH 113
                                                                                114 FYWIGLSYSEEHTAWLWENGSALSQYLFPSFETFKPKNCIAYNSKGNALDESCETKNRYI 173
                                                                                                                                             174 CKQQL 178
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                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21158386; PubMed=11261935;
Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rhesus monkey decidua.";
Immunogenetics 53:69-73(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PSSO041; C_TYPE_LECTIN_2; 1.
Antigen; PSCOPPOOF; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                ΰ
                                                                                                                                                                                                                -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20322487; PubMed=10866118;
Labonte M.L., Levy D.B., Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 163.5; DB 1; Length 179; Pred. No. 4.7e-09;
                                                                                                                                                                                                                                                                                                                                                                  Isold=09MXZV9-2. Sequence=VSP_003055;
Name=3; Synonyms=CD94 alt;
Isold=09MXZV9-3; Sequence=VSP_003054;
-!- TISSUB SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LONG FORM) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06212B4494527F07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> LQ (In isoform 2). /FTId=VSP 003055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   003054.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                           IsoId=Q9MZK9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                             [mmunogenetics 51:496-499(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF190931; AAF74527.1; -- EMBL; AF190932; AAF74528.1; -- EMBL; AF190933; AAF74529.1; -- EMBL; AF294886; AAG34498.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_c; 1. SMART; SMO0034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                           Name=1; Synonyms=CD94-A;
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72
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166
83
132
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179 AA;
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Best Local Similarity
Matches 39; Conserv
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TRANSMEM
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                                                                              and D.";
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SEQUENCE FROM N.A.
MEDLINES-R726056; PubMed=3597443;
Halberg D.F., Wager R.E., Farrell D.C., Hildreth J., Quesenberry M.S.,
Loeb J.A., Holland E.C., Drickamer K.;
"Major Holland E.C., Drickamer K.;
"Major and minor forms of the rat liver asialoglycoprotein receptor
are independent galactose-binding proteins. Primary structure and
glycosylation heterogeneity of minor receptor forms.";
J. Biol. Chem. 262:9828-9838 (1987).
                                       01-AUG-1988 (Rel. 08, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Asialoglycoprotein receptor R2/3 (Hepatic lectin 2/3) (RHL-2) (ASGP-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminal galactose and N-acetylgalactosamine units. After ligand binding to the receptor, the resulting complex is internalized and transported to a sorting organelle, where receptor and ligand are disassociated. The receptor then returns to the cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANBOUS: Calcium is required for ligand binding.
-!- MISCELLANBOUS: TWO types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, having a relative abundance of 4:1. RHL-2 and RHL-3 only differs in thir carbohydrate structures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=89170119; PubMed=3234178;
Sanford J.P., Elliott R.W., Doyle D.;
"Asialoglycoprotein receptor genes are linked on chromosome 11 in the
                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drickamer K., Mamon J.F., Binns G., Leung J.O.;
"Primary structure of the rat liver asialoglycoprotein receptor.
"Primary structure of the rat liver asialoglycoprotein receptor.
J. Biol. Chem. 259:770-778(1984).
-!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to which the terminal sialic acid residue on their complex carbohydrate moieties has been removed. The receptor recognizes
                                                                                                                                                                                                                                                                                           MEDLINE=87257885; PubMed=3600647; McPhaul M., Berg P.; "Identification and characterization of cDNA clones encoding two
                                                                                                                                                                                                                                                                                                                                                           the asialoglycoprotein
  301 AA
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                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 7:1841-1847(1987).
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STANDARD;
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                                                                                                                                             ASGR2 OR ASGR-2
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  LECI RAT
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Gaps

9;

Indels

58;

19; Mismatches

39; Conservative

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SEQUENCE FROM N.A.
                                                                                                                                                         STRAIN=C57BL/6J;
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DISULFID
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                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GVNLFQEYVGEDFYWIGLRDIDG-WRWEDGPALSLSILSNSVVQ------KCG 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deccini, organization.
Calcium; Signal-anchor; Phosphorylation.
DOMAIN 158 CYTOPLASMIC (POTENTIAL).
TO SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Natural killer cell sizece protein Pl-40 (NKR-Pl 40) (NKR-Pl.9)
KLRBIC OR LYSSC OR LYSS-C.
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                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL).

EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
R - A (IN REF. 2 AND 3).
C -> W (IN REF. 2 AND 3).
 SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3C2315E642D71279 CRC64;
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                                                                                                                                                                                  EMBL; M16347; AAA42038.1; --
EMBL; J02762; AAA41522.1; --
EMBL; X07636; CAA30476.1; --
FIRS, E28462; LNRT2.
HSSP; P06734; IHLI.
INTERPO; IPR00233; ANTIFREEZEII.
INTERPO; IPR002333 ANTIFREEZEII.
Ffan; PP00059; lectin C;
Ffan; PP00059; lectin C;
Ffan; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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P27814;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPQDWILHEDKCFHVSQVSNTWEEGQADCGRKGATLLLIQDQEELRFLLDSIKEKYNSFW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFFPDNQGVNLFQEYVGEDF--YW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 IGLR----DIDGWRWEDGPALSLSILSNSVVQK---CGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLALKLSCAGLILLV----LTLIGMSVLVRVLVQKPSREKCC---VFIQENINKTIVNLE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 KAVLHRPCVSYLVMVALGLLTVILMSLLLY-----QRTLCCGSKGFMCSQCSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                        Giorda R., Trucco M., "Mouse NKR-P1. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
C.TYPE LECTIVE LECTIVE
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                              MEDLINE=92373004, PubMed=1506685, Ryan J.C., Turck J., Niemi B.C., Yokoyama W.M., Seaman W.E., Wolecular cloning of the NK1.1 antigen, a member of the NKR-P1 family of natural killer call activation molecules.", J. Immunol. 149:1631-1635(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 159.5; DB 1; Length 220; 25.3%; Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:107538; KIrblc.
MGD; MGI:107538; KIrblc.
InterPro; IPR002535; AntifreezeII.
InterPro; IPR00359; Lectin_C.
Pfam; PR00559; lectin_C.
PRNUTS; PR00356; ANTIFREEZEII.
SMART; SM0034; CLECT; 1.
PROSITE; PS00615; C TYPE_LECTIN_I; FALSE_NEG.
PROSITE; PS00615; C TYPE_LECTIN_Z; 1.
Glycorotein; Antigen; Transmembrane; Signal-anchor; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                -:- FUNCTION: May function as signal-transmitting receptor.
-:- SUNCELULAR LOCATION: Type II membrane protein.
-:- TISSUE SPECIFICITY: Natural killer cells.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8A160B1DED46398F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
MEDLINE=91349596; PubMed=1880421;
                                                                                                                   Immunol. 147:1701-1708(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 EX
212 C-
212 C-
207 BY
199 BY
199 BY
183 N-
166 N-
143 N-
24771 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M77678; AAA39824.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
90
91
119
119
186
186
163
183
220 AA;
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                                                                                                                                                                                SEQUENCE FROM N.A.
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RESULT 8
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 LALVGMSILVRVLVQKPSVEPCRVLIQENLSKTGSPAKL----KCPKDWLSHRDKCFHV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 SMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVG--EDFYWIGLR---DIDGWRWE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 LVMVALGLLTVILMS-----LLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                       15-MAR-2004 (Rel. 43, Last annotation update)
Natural killer cell surface protein Pl-3.2.3 (NKR-Pl 3.2.3) (Antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Gaps
                                                                                                                                                                      MEDLINE-90378305; Pubmed=2399464; MEDLINE-90378305; Pubmed=2399464; Giorda R., Rudert W.A., Vavassori C., Chambers W.H., Hiserodt J.C., Trucco M.; MRR-Pl, a signal transduction molecule on natural killer cells."; WRR-Pl, a signal transduction molecule on natural killer cells."; FOUCTION: Mediates transmembrane signaling in natural killer (NK) cells and so may act as a receptor able to selectively trigger NK cell activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
DOMAIN 1 1 43 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Natural killer cells.
-!- MISCELLANFOUS: Ligand binding may be calcium dependent.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FCD12B212DDF4330 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 1.5e-08; 33; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMO0034; CLECT; 1.
PROSITE; PSO0615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
                          223 AA.
                                                             (Rel. 23, Last sequence update) (Rel. 43, Last annotation under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 159.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΒY
                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seq
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin c; 1. PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M62891; AAA41710.1; -.
PIR; A35917; A35917.
HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Conservative
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 1
223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DISULFID
DISULFID
                       NK13 RAT
P27471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
RESULT 7
             NK13_RAT
                                    q
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RX STRAIN=WIN, INSUBELINEL;

RA MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D. Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Distchenkor L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Paches S., McTupy R.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,

RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schmutz J., Marra M.A.;

RA Schnerch A., Schmutz J., Marra M.A.;

RY "Generation and initial analysis of more than 15,000 full-length

RY Human and mouse cDNA sequences.";

Proc. Natl. Complex Complex Complex

"Wich the perminal sialic acid residue on thear complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             terminal galactose and N-acetylgalactosamine units. After ligand binding to the receptor, the resulting complex is internalized and transported to a sorting organelle, where receptor and ligand are disassociated. The receptor then returns to the cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which the terminal stalic acid residue on their complex carbohydrate moieties has been removed. The receptor recognizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor genes during mammalian evolution.", Biochim. Biophys. Acta 1087:259-261(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
                                                      169 NGSTLNSDVLSITGDTEKDSCASVSODKVLSESCDSDNIWVCOKEL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: Calcium is required for ligand binding. SIMILARITY: Contains 1 C-type lectin family domain.
145 DGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL
                                                                                                                                                                                                                                                                                                                                         301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91027942; PubMed=2223888;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanford J.P., Doyle D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASGR2 OR ASGR-2.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                    LECI MOUSE
P24721;
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TISSUE SPECIFICITY: Natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                     213
110
211
203
203
115
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                             202
216 AA;
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                         73
98
99
127
127
1189
                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKGD HUMAN
                                                                                                                                                                                                                                     DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells."
                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                               213 BQDFVVKHRSQFHIWIGLTDRDGSWKWVDGTDYRSNYRNWAFTQPDNWQGHEQGGGEDCA 272
                                                                                                                                                                                                                                                                                                                                                        RTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQ 117
                                                                                                                                                                                                                                                                                                                                                                            153 ŘÍĽTCQLAYFQSNGTECCPVNWVEFGGSCYWFSRDGLTWAEADQYCQLENAHLLVINSRE 212
                                                                                                                                                                                                                                                                                                                                                                                                 -----KCG 163
                                                                                                           PRINT, SMO034; CLECT; 1.

SMART; SM0034; CTYPE LECTIN 1; 1.

PROSITE; PS0041; C_TYPE LECTIN 2; 1.

Lectin, Glycoprotein; Receptor; Endocytosis; Transmembrane;
Calcium; Signal-anchor; Phosphorylation.

CATOPLASMIC (POTENTIAL).

79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics 51:496-499(2000).
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC
class I HAA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBDMIT: Can form disulfide-bonded heterodimer with CD94.
                                                                                                                                                                                                   EXTRACELLUIAR (POTENTIAL).
C.TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N.LINKED (GLCNAC. . .) (POTENTIAL).
N.LINKED (GLCNAC. . .) (POTENTIAL).
N.LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20322487; PubMed=10865118; LaBonte M.L., Levy D.B., Letvin N.L.; Carbin V.L.; Levy D.B., Letvin monkey CD94/NKG2 family members and "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, E
                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ž
                                                                                                                                                                                                                                                                                                             Score 159.5; DB 1; Length 301; Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-D type II integral membrane protein (NKG2-D activating)
                                                                                                                                                                                                                                                                                                                                   67; Indels
                                                                                                                                                                                                                                                                                        3A29F1AFBA68F298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 GVNLFQEYVGEDFYWIGLRDIDG-WRWEDGPALSLSILSNSVVQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Type II membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 AA
                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            164 TIHRCG-LHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELLSDGHWNDNFCQQVNRWVCEK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                         MGD; MGI:88082; Asgr2.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin C.
InterPro; IPR005640; lectin C.
Pfam; PF00059; lectin c; 1.
Pfam; PF00554; lectin N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor) (NK cell receptor D).
                                                                                                        PRINTS; PR00356; ANTIFREZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                         34907 MW;
                                                                                                                                                                                                                                                                                                              15.4%;
, X53042; CAA37211.1; -.; BC011197; AAH11197.1; S13165; S13165.
                                                                                                                                                                                                                                                                                                                                   38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                       301
295
181
2293
285
285
97
165
                               P06734; 1HLI.
                                                                                                                                                                                                                                                                                         301 AA;
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                       80
169
170
198
271
97
165
298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKGD MACMU
                                                                                                                                                                                                               DOMAIN
DISULFID
                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                 118
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                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09MZJ7;
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKGD_MACMU
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 MEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDI---DGWRWEDGP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 NESKOWYESQASCMSQNASLLKVYSKEDQDLLK--LVKSYHWMGLVHIPTNGSWQWEDGS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 VMVALGLLTVILMSL------LLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91178434; PubMed=2007850; Houchins U.P., Yabe T., McSherry C., Bach F.H.; Houchins U.P., Yabe T., McSherry C., a family of related cDNA clones encoding type II integral membrane proteins on human natural killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACEMENT.

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKG2-D type II integral membrane protein (NKG2-D activating NK receptor) (NK cell receptor D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.3%; Score 159; DB 1; Length 216; 26.4%; Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 ALSLSILSNSVVQKCGTIHRCGLHASS-----CEVALQWIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 ILSPNLLTIIEMQK----GDCALYASSFKGYIENCSIPNTYIC 211
!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A44883F31400DEAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exp. Med. 173:1017-1020(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                             EMBL, AF190943; AAF74539.1; -.
InterPro; IFR001304; Lectin C.
Pfam; PF00059; lectin C; 1.
SMART; SM00034; CLBCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Polymorphism.
DOMAIN 1 51
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                                                                                                                                                                                                                                                                                                                                                                                                                      RY SEQUENCE FROM N.H. A. S. SEGURE D.H., Derge J.G., BLUINE-22388257; PubMed=12477932; RA Strausberg R.L., Fahigold B.A., Grouse L.H., Derge J.G., Strausberg R.L., Fahigold B.A., Grouse L.H., Derge J.G., Altasner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Rapkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Shevchenko Y., Bouffard G.G., Rhaterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Rutterfield Y.S.N., Marsha M., Man and mouse cDNA sequences ""

R. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ""

R. FUCC. Natl. Acad. Sci. U.S.A. 99:16899-16903(202).

C. - FUNCTION: Plays a role as a receptor for the recognition of MHC C. Subcriulan Local Sci. U.S.A. 99:16890-16903(202).

C. - Subcriulan Specificity: Natural killer cells.

C. - Subcriulan Specificity: Natural killer cells.

C. - TISSUE Specificity: Natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GG:0005887; C:integral to plasma membrane; TAS.
GO:0004872; F:receptor activity; TAS.
GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
                Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C., Lehrach H., Hofer E., Francis F.; "The genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex."; Immunogenetics 48:163-173(1998).
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT THR-72.
MEDLINE=21623889; PubMed=11751968;
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
Cleland S., Guechlein L.A., Uhrberg M., Parham P.;
"Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                         Kothapalli R., Kusmartseva I., Loughran T.P. Jr.; Tdentification and characterization of the NKG2D gene from large granular lymphocytic leukemia [LGL] cells."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ001687; CAA04925.1; -.
AJ001688; CAA04925.1; JOINED.
AJ001689; CAA04925.1; JOINED.
MEDLINE=98350122; PubMed=9683661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF461811, AAL65233.1; --
EMBL, AF260135, AAF86973.1; --
EMBL, AF260136; AAF86974.1; --
EMBL, BC039836; AAH39836.1; --
                                                                                                                                                                                                                                                                                                                                                                         Immunol. 168:240-252(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X54870; CAA38652.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1HYR; 23-MAY-01.
1KCG; 09-JAN-02.
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        NKG2 genes.'
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65 IRFIIMVA--IWSAVFLNSLFNQEVQIPLTE----SYCGPCPKNWICYKNNCYOFFDESK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 DWNSSLKFCADKGSHLLITFPDNQGVNLFQEYVGEDFYWIGLRDI---DGWRWEDGPALSL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 NWYESQASCMSQNASLLKVYSKEDQDLLK--LVKSYHWMGLVHIPTNGSWQWEDGSILSP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 VSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR 94
                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96011848; PubMed=7589107;
Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
                                                     Pfam; PF00059; lectin_c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM0034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                   C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q13241; O43321; O43773; Q9UBE3; Q9UBEQ0; U-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 35, Last annotation update) 15-MAR-2014 (Rel. 43, Last annotation update) 16-MAR-2014 (Rel. 43, Last annotation update) 17-MAR-2014 (Rel. 43, Last annotation update) 17-MAR-2014 (Rel. 43, Last annotation update) 18-MAR-2014 (Rel. 43, Last annotation update) (Killer cell Recin-like receptor subfamily D, member 1) (KP43).
                                                                                                                                                                                                                                                                                                                                                         NKED (GLCNAC. . .) (POTENTIAL)
T (in allele NKG2-D*02)
B=VAR 013295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98139529; PubMed=9472066;
Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
Lehrach H., Francis F., Lopez-Botet M.;
"Structure of the human CD94 C-Type lectin gene.";
Immunogenetics 47:305-309(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            C22F6BD533D7800E CRC64;
                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SILSNSVVQKCGTIHRCGLHASS-----CEVALQWIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.2%; Score 157; DB 1;
Best Local Similarity 26.4%; Pred. No. 2.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 AA.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Mismatches
                                                                                                                                                               Glycoprotein; Polymorphism; 3D-structure.
DOMAIN
                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                       216
213
110
211
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131
163
202
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                                                                                                                                                                                                                                                   73
98
127
127
131
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CARBOHYD
VARIANT
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Strausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,

Rlausner R. D., Collins F. S., Wagner L., Shenmen C. M., Schuler G. D.,

Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Blant N. K.,

Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raba S. S., Loquellano N. A., Peters G. J., Abramson R. D., Milahay S. J.,

Raba S. S., Worley N. J., McKernan K. J., Malek J. A., Gumarathe P. H.,

Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,

Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,

Richards S., Worley M., Sodergren E. J. L. X., Gibbs R. A.,

Nilalon D. K., Murny D. M., Sodergren E. J., Lu X., Gibbs R. A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R. M.,

Schnerch A., Schein J. S., Jones S. J. M., Marra M. A.;

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U. S. A., 99:16899-16903 (2002).

Li FUNCTION: Plays a role as a receptor for the recognition of MHC

C. !- FUNCTION: Plays a role as a receptor for the recognition of C. I. FUNCTION: Plays a role as a receptor for the recognition of MHC

C. !- FUNCTION: Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays a role as a receptor for the recognition of Function Plays
                                                                                                                                                 Tadokoro K.,
                                                                                              SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=98267245; PubMed=9601951;
Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T.,
Tohma S., Inoue T., Yamamoto K., Juji T.;
"A alternatively spliced form of the human CD94 gene.";
Immunogenetics 48:87-88(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoid=Q13241-3; Sequence=VSP 003052;
TISSUE SPECIFICITY: Natural killer cells.
SIMILARITY: Contains 1 C-type lectin family domain.
DATABASE: NAME-PROW; NOTE=CD quide CD94 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
                                                  Biassoni K.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type II membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2; Synonyms=CD94-B;
IsoId=Q13241-2; Sequence=VSP_003053;
Name=3; Synonyms=CD94 alt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q13241-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932;
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EMBL; Y14287; CAA74663.1; -.
EMBL; Y14288; CAA74663.1; JOINED.
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AJ000001; CAA03845.1; -.
AB009597; BAA24450.1; -.
                                                                                                                                                                                                                                                      FROM N.A. (ISOFORM 1).
                      SEQUENCE FROM N.A. (ISOFORM 2).
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MIM; 602894; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
MANYKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. .; TAK
GO; GO:000766; P:call surface receptor linked signal transdu. .; TAK
InterPro; IPR001304; Lectin_C.
FEAM; PR00059; lectin_c; I.
FROSITE; SR00064; CIPPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; CIPPE LECTIN 2; 1.
PROSITE; PS50041; CIPPE LECTIN 2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; 3D-structure.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 IDGWRWEDGPALSLSILSNSV---VQKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 HTAWLWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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10-OCT-2003 (Rel. 42, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1).
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SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=20350666; PubMed=10894168;

Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,

Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,

Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
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/FTId=VSP_003052.
L -> LQ (in isoform 2).
/FTId=VSP_003053.
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28-FEB-2003 (Rel. 41, Last seq
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                        InterPro; IRR01304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLET; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM
                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
       J. Immunol. 168:240-252(2002).
-!- FUNCTION: Plays a role as a receptor for the recognition of WHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 HTAWLWENGSALSOYLFPSFETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 IDGWRWEDGPALSLSILSNSVV---QKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (FOTENTIAL).
N-LINKED (GLCNAC. .) (FOTENTIAL).
L -> LQ (in isoform 2).
/FTIG=VSP_003056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.0%; Score 155; DB 1; Length 179; 27.0%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Macrophage asialoglycoprotein-binding protein 1 (M-ASGP-BP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Indels
                                                                                                                          Name=2; Synonyms=CD94-B; IsoId=Q9MZ41-2; Sequence=VSP 003056; -:- TISSUE SPECIFICITY: Natural killer cells. -:- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7244D99E8D9587E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                           -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERRATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1; Synonyms=CD94-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 AA
                                                                                                                     IsoId=Q9MZ41-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                       EMBL; AF259054; AAF86964.1; -.
HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20493 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                          Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       32
98
61
89
152
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMGL MOUSE
P49300;
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Matches
NKG2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oda S., Sato M., Toyoshima S., Osawa T.;
"Purification and characterization of a lectin-like molecule specific for galactose/N-acetyl-galactosamine from tumoricidal macrophages.";
J. Biochem. 104:600-665(1988).
-!- FUNCTION: Recognizes terminal galactose and N-acetylgalactosamine units. May participate in the interaction between tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
Macrophage galactose/N-acetylgalactosamine-specific lectin) (MMGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                      mont on .....
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                               MEDLINE-92268032; PubMed=1587794; Sato M., Kawakamyl K., Osawa T., Toyoshima S.; Kawakamyl K., Osawa T., Toyoshima S.; Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalactosamine-specific lectin on mouse tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL) .
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C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GICHAC. . . ) (POTENTIAL).
N-LINKED (GICHAC. . . ) (FORENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macrophages.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LINKED (GLCNAC. . .) (Post 3F79CD12C34F5BCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; Score 154.5; DB 1
27.8%; Pred. No. 6.4e-08;
iive 19; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JX0209; JX0209.
HSSP; P06734; IHII.
MGD; MGI:96975; Mg11.
InterPro; IPR002353; AntifreeZell.
InterPro; IPR001304; Lectin C.
InterPro; IPR065640; lectin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C3H/HeN;
MEDLINE=89197865; PubMed=3241002;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 102-120 AND 137-151.
                                                                                                                                                                                                                                                                                                                                                                J. Biochem. 111:331-336(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34596 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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298
184
296
288
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 AA;
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Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 HCYYFSMEKRDWNSSLKFCADKGSHLLIFPDNQGVNLFQEYVGEDFYWIGLRDID---GW 141
 -KCGTIHRCG-LHASS 174
                                  228 VSWIGLTDONGPWRWVDGTDFEKGFKNWAPLOPDNWFGHCLGGGEDCAHITTGGPWNDDV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --CKEGWVGYNK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCVSYLVMVALGLLTVILMS-----LLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-116 FROM N.A.
STRAIN=FP-9 / Isolate HP-438;
MEDLINE=88229622; PubMed=2836348;
TomLey F., Binns M., Campbell J., Boursnell M.E.G.;
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                                                                                           Fowlpox virus (FPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zsak L., Kutish G.F., Rock D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 154; DB 1; Length 163; 22.9%; Pred. No. 3.7e-08; tive 31; Mismatches 65; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 RWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of fowlpox virus.";
J. Gen. Virol. 69:1025-1040(1988).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AA; 18635 MW; 5156DC8928855532 CRC64;
                                                                                                                                                                                             V239 FOWPV STANDARD; PRT; 163 AA. P14371; Q9J500; O1-JAN-1990 (Rel. 13, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Putative C-type lectin protein FPV239 (BamHI-ORF8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFam, PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TYPE LECTIN.
130 FYWIGLRDIDG-WRWEDGPALSLSILSNSVVQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | ::: | : :| | : :| | PCGS--IIIVLSVFVIILSTRPPVPPDIKILY
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20193820; PubMed=10729156; Afonso C.L., Tulman B.R., iu Z., Zs "The genome of fowlpox virus."; J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF198100; AAF44583.1; -.
EMBL; D00295; BAA00203.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, H29963, WMVZF8.
HSSP, P05140, 2AFP.
InterPro, IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Lectin.
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Conservative 3
                                                                                                        288 CORTFRWICEMKL 300
                                                                        CEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                 Avipoxvirus
                                                                        175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                  Cell activation anigens...

Eur. J. Immunol. 23:1643-1648(1993).

-!- FUNCTION: Involved in lymphocyte proliferation and functions as a signal transmitting receptor in lymphocytes, natural killer (NK) cells, and platelets.

-!- SUBGNIT: Homodimer; disulfide-linked.

-!- SUBCELIULAR LOCATION: Type II membrane protein.

-!- STRUE SPECIFICITY: EXPRESSED ON THE SUBRACE OF ACTIVATED T CELLS, B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS AND PLATELETS.

-!- DEVELOPMENTAL STAGE: Earliest inducible cell surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                   MEDLINE=93314711; PubMed=8100776;
Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
                                                                                                                                                                                                                                                                                                                                                                    "Molecular characterization of the early activation antigen CD69: a type II membrane glycoprotein related to a family of natural killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
C.TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N.LINKED (GLCNAC. .) (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acquired during lymphoid activation.
-!- INDUCTION: By the activation of T lymphocytes.
-!- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE THYMOCYTES AND ACTIVATED T LYMPHOCYTES (BY SIMILARITY).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001353; Antifreezell.
InterPro; IPR001304; Lectin_C.
Pfam; PR0059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C.TYPE LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein; Phosphorylation.
39F8E4941D36D4F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                               A.
                                                                                               199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L23638; -; NOT ANNOTATED_CDS. MGD; MGI:88343; Cd69.
                                                                                               PRT;
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195 C-
194 B1
186 B1
150 N-
160 N-
22517 MW,
                                                                                                                                                                           Early activation antigen CD69.
                                                                                               STANDARD;
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61
                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                         Alderson M.R.;
                                                                                               MOUSE
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                                                               RESULT 15
CD69_MOUSE
ID _CD69_M
                                                                                                                                                                                            CD69.
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Search completed: August 10, 2004, 16:17:00 Job time: 7.32035 secs

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August 10, 2004, 16:11:32; Search time 32.6089 Seconds (without alignments) 1819.059 Million cell updates/sec
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1 MADNSIYSTLELPAAPRVQD.....GLHASSCEVALQWICEKVLP 188
                                                                                                                                                                                                                                                                                                                           1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                      1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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sp_human:*
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sp_unclassified:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q64335 rattus norv	088713 mus musculu	075613 homo sapien	Q96e93 homo sapien	043198 homo sapien	Q9d403 mus musculu	Q90636 gallus gall	Q9nzsl homo sapien	Ognzs2 homo sapien	Q802s8 gallus gall	Q8mi05 macaca fasc	Q8bru4 mus musculu	Q8hy11 hylobates s	O54708 mus musculu	O54707 mus musculu	Q9uhp7 homo sapien
SUMMAKIES		ID	Q64335	088713	075613	О96Е93	043198			-	_		•		Q8HY11			
		DB	11	11	4	4	4	11	13	4	4	13	Ø	11	9	11	11	4
		Match Length DB	188	188	189	195	189	275	257	181	231	200	231	238	422	179	179	191
	م مامرد	Match	100.0	80.9	52.7	52.3	50.7	19.4	17.8	17.2	17.2	17.1	17.1	17.1	17.0	16.9	16.9	16.8
		Score	1036	838	545.5	541.5	525.5	201.5	184	178	178	177.5	177	177	176.5	175	175	174.5
	Result	No.	н	2	3	4	_C	9	7	80	6	10	11	12	13	14	15	16

Q8cbb4 mus musculu Q8hy12 hylobates 1 Q8hy10 hylobates c Q91zw7 mus musculu Q91zw7 mus musculu Q91zw7 mus musculu Q91zw5 mus musculu Q91y25 mus musculu Q91y25 mus musculu Q21y3 mus musculu Q2593 mus musculu Q2594 mus musculu Q8hy17 hongo pygma Q91zw8 mus musculu Q8hy16 homo sapien Q8my16 homo sapien Q8my10 pongo pygma Q91zw8 mus musculu Q89p32 mus musculu Q89p32 mus musculu Q99p32 mus musculu Q99p32 mus musculu Q99p32 mus musculu Q99p32 mus musculu Q99p32 mus musculu Q99p32 mus musculu Q99p14 mus musculu Q99p14 mus musculu Q99p14 mus musculu Q99124 mus musculu Q99124 mus musculu Q99124 mus musculu Q99124 mus musculu Q99124 mus musculu	D. D.
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                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPRAGUE DAWLEY, TISSUE=Testis,
Bocek Jr P., Guthmann M.D., Pecht I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                 188 AA.
                                                                                                                                  Created)
                                                                 PRT;
                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25,
                                                                 PRELIMINARY;
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Q64335;
RESULT 1
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CGGSKDSTCSHCPSCPILMTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLIFFPDNQGVK 120
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                                                                                                                                                                  CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99077194; PubMed=8862378;
MEDLINE=99077194; PubMed=8862378;
MEDLINE=99077194; PubMed=8862378;
MEDLINE=99077194; Vance R.E., Raulet D.H.;
"2Fl antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1998).
EMBL; AF081675; AAC32200.1; --
GO; GO:0005529; F: sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
Pfam; PF000559; lectin_C.
Pfam; PF000559; Lectin_C.
SMART; SM00034; CLECT; 1.
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                                      1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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                    MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Butcher S., Arney K.L., Cook G.P.;
"MARA-L, an ITIM-contraining receptor encoded by the lecomplex and expressed by basophils and NK cells.";
Eur. J. Immunol. 28:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) ITIM-containing receptor MAFA-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.7%; Score 545.5; DB 4;
55.1%; Pred. No. 3.1e-50;
ive 28; Mismatches 55;
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Best Local Similarity
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01-OCT-2003
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                                                                                                                                CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDDNQGVN 120
                                                                                                                                                                                                LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
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SEQUENCE FROM N.A.
SIGUINNE.B-17 SCID;
MEDLINE=99071394; PubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
"2F1 antigen, the mouse homolog of the rat '$1', is a lectin-like type "II transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and physical mapping of the (KLRG1), the mouse homologue
                                                                                               MADNS IYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                  MADNS IYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1999 (TrEMBLrel. 11, Last sequence update)
01-AUG-1999 (TrEMBLrel. 12, Last annotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
KLRG1 OR MAFA.
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                                      Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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     DB 11; Length 188;
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                                   Indels
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
   Score 1036; DB 11;
Pred. No. 1e-102;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.9%; Score 838; DB 11;
80.7%; Pred. No. 1.6e-81;
ive 15; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                         188 AA
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STRAIN=129/SvevTACfBr; TISSUE=Spleen;
MEDLINE=21115136; PubMed=11220622;
Woehringer D., Kaufmann M., Pircher H.;
"Genomic structure, alternative splicing, killer cell lectin-like receptor G1 gene (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                         PRT;
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BMBL; AP097357; AAD00718.1; -.

EMBL; AJ010751; CAA09342.1; -.

EMBL; AF317727; AAK40082.1; -.
   100.0%; Sc
100.0%; Pr
:ive 0;
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Blaser C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.73
Matches 151; Conservative
Query Match
Best Local Similarity 100.
Matches 188; Conservative
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SEQUENCE 188 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQGSNYSTCASCPSCPDRWMXYGNHCYYFSVEEXDMNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ILQVFLSEAFCWIGLRNNSGWRWEDGSPINFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLS-ILSNSVVQKCGTIHRCGLHASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to killer cell lectin-like receptor subfamily G, member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Bone marrow;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012621; AAH12621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 AA; 21831 MW; 178EE98E08EEC473 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 06, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
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"Human MAFA has alternatively spliced variants.";
Biochim. Biophys. Acta 1399:209-212(1998).
EMBL; AF034952; AAC34731.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.3%; Score 541.5; DB 4 54.8%; Pred. No. 8.6e-50; iive 28; Mismatches 55
                                                            195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0004872; F:receptor activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mast cell function-associated antigen
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                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 54.8
Matches 102; Conservative
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                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC: 6380; KLRG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                          (Human)
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                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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SEOUENCE 195 A
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01-JUN-1998
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XE STRAIN-GSTBL/64; TISSUE-Testis;

X RAWAI G. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S.,

A Azawa X., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

X Gadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

X Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

X Kadota K., Matsudi F., Sizuki R., Tomita M., Wagner L., Washio T.,

X Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

R Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Uyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Whinshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanshar-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LLQVFLSEAFCWIGLRINSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLS-ILSNSVVQKCGTIHRCGLHASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                          signal transdu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 189;
GO; GO:0003793; F:defense/immunity protein activity; TAS. GO; GO:0004872; F:tectin: TAS. GO; GO:0004872; F:tectin: TAS. GO; GO:0004872; F:teceptor activity; TAS. GO; GO:0007166; P:cell surface receptor linked signal tran GO; GO:0006968; P:cellular defense response; TAS. GO; GO:0006954; P:inflammatory response; TAS. InterPro; IRRO1304; Lectin.C. Pfam; PF00059; lectin.c; 1. SMRAT; SMO034; CLECT; 1. SMRAT; SMO034; CLECT; 1. SRO1304; CLECT; 1. SEQUENCE 189 AA; 21079 MW; ISE042AD40B2B4F6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.7%; Score 525.5; DB 4.53.5%; Pred. No. 4.3e-48; iive 29; Mismatches 57.
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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WRWEDGPAL 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MADNSIYSTLELPAAPRVQ-DDSRWKVK---AVLHRPCVSYLVMVAL----GLLTVILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : : | : | : | : | : | : | : : | : | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
Fernandez-Ruiz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                 KRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human KIRFI, a novel member of the killer cell lectin-like gene family; molecular characterization, genomic structure, mapping to the NK gene complex and expression analysis."; Bur. J. Immunol. 30:568-576(2000).

EMBL; AR175207; AAF37805.1; -..
GO; GO:0016020; C:membrane; TAS.
GO; GO:0016020; C:membrane; TAS.
InterPro; IRR001104; Lectin_C.
Ffam; PF00059; lectin_C.
Ffam; PF00059; lectin_C.
PRART; SM00034; CIECT; 1.
PROSITE: PS50041; C_INECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 17.2%; Score 178; DB 4; Length 18 I Similarity 25.0%; Pred. No. 6.2e-11; 51; Conservative 32; Mismatches 77; Indels
                                                                                                                                                   : : | : | : | : | 207 T----NRPVFELRGGGRCAYINGDGISSALCHSEKFWVCSR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AA; 21204 MW; 64642240CAE1E551 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
Lectin-like receptor F1 (Activating coreceptor NKp80).
KLRF1 OR ML/KLRF1.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amotation update)
Lectin-like receptor F1, splice variant 1 KLRF1-s1.
KLRF1.
                                                                                                                         SLSILSNSVVQ-----KCGTIHRCGLHASSCEVALQWICEK
                                                                                                                                                                                                                                                                                   181 AA.
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| CAAIKESKIFSETCSSVFKWICQ 180
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                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              QR----TLCCGSKGFMC----SQCSRCPNLWMRNGSHCYYFSM-EKRDWNSSLKFCADKG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 SHLLTFPDNQGVNLFQEYVG--EDFYWIGLR-DIDG--WRWEDGPALSLSILSNSVV--- 159
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MEDLINE=94164691; PubMed=8119728;
Bernot A., Zoorob R., Auffray C.;
"Linkage of a new member of the lectin supergene family to the chicken
                                                                                                                                                                                                                                                                                                             1 MADNSIYSTLELPAAPRVQ-------DDSRWKVKAVLHRPCVSYLVMVALGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                    19.4%; Score 201.5; DB 11; Length 275; 23.4%; Pred. No. 3.1e-13; ive 40; Mismatches 77; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
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MGD; MGI:1918433; 4933425B16RiK.
GO; GO:005529; F:sugar binding; IEA.
InterPro; IRR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PSG0041; C TYPE L.
SEQUENCE 275 AA; 31360 MW; C9792BA25C8B5CC2 CRC64;
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SEQUENCE 257 AA; 28814 MW; G67EA483F4E85333 CRC64;
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Last annotation update)
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                                                                                                                                                                                                     23.4%; Prea. nc.
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PIR; I50146; I50146;
GO; GO:0005529; F:sugar binding; IEA.
INTERPRO; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                 63; Conservative
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17.5.
Gallus gallus (Chicken).
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Best Local Similarity
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89 SKEENDWNSSREHCNAHGASLATIGSAEEMDFMMRFQGPANCWIGLHREEEDAQWTWSDG 148
             "Analysis of part of the chicken Rfp-Y region reveals two novel lectin genes, the first complete genomic sequence of a class I alpha-chain gene, a truncated class II beta-chain gene, and a large CR1 repeat."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ277927; CAD61336.1; ---
GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007527; P:hetrophilic cell adhesion; IEA.

InterPro; IPR002353; AntifreezeII.

InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CSRCPNLWMRNGSHCYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 VCAALGALILVLVVI-----STVCRQVPVPPFPDFAHACPNAWVGFQGKCYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 SMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL----RDIDGWRWEDG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 200;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ426430; CAD19994-1; -..
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 TAFTNWFELRGGG---RCAYLNGDRISSSLCHLHKHWVCSR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 PALS--LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                               22573 MW; 23AA950D113349B8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  17.1%; Score 177.5; DB 13.26.1%; Pred. No. 7.9e-11; ive 24; Mismatches 66.
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17.1%; Score 177; DB 6;
Best Local Similarity 23.5%; Pred. No. 1.1e-10;
Matches 56; Conservative 32; Mismatches 88;
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Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                              PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 INFTSLKMTWTWVDGSPIDSKIFFIKGPAKENS----CAAIKESKIFSETCSSVFKWICQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 SLILLVSQGVLLKCQKGSCSNATQYEDTGDLKVNNGTRRNISNKDLCASRS--ADQTVLC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 PNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE-DFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRDID---GWRWEDGPALSLSIL----SNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-2115(0889) PubMed=11265639;
Vitale M., Falco M., Castriconi R., Parolini S., Zambello R.,
Vitale M., Falco M., Castriconi R., Parolini S., Zambello R.,
Vitale M., Falco M., Castriconi R., Bortino C., Moretta J., Moretta A.)

"Identification of NKp80, a novel triggering molecule expressed by human natural killer cells.";

EMBL; AF175206; AAF37804.1; -.

EMBL; A7305370; CAC29425.1; -.

EMBL; A7305370; CAC29425.1; -.

EMBL; A7305370; CAC29425.1; -.

Gonew; HGNC:13342; KLRF1.

GO, GO:0005887; Cintegral to plasma membrane; TAS.

GO; GO:0004888; Fitransmembrane receptor activity; TAS.

GO; GO:0004688; Fitransmembrane receptor activity; TAS.

GO; GO:000166; P:cell surface receptor linked signal transdu. .; TAS.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                "Human KLRF1, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis.";

Bur. J. Immunol. 30:568-576(2000).
                                                                                                                        MEDLINE=20135860; PubMed=10671213;
Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.
Fernandez-Ruiz E.;
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.2%; Score 178; DB 4; Length 231; 23.3%; Pred. No. 8.3e-11; ive 34; Mismatches 84; Indels 6
                     Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A2F7BE6D4341AFDE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AA; 26562 MW;
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Eukaryota; Metazoa;
                        Eutheria;
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                                             NCBI_TaxID=9606;
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01-OCT-2003
                        Mammalia;
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                                                                                             128
                  SLILLVSQGVLLKCQKGSHSNTTEHEDIGDLKMNNGTRRNTSNKDLCVSRSADQTVLCQS 116
                                                                   LWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFPDNQGVNLFQEYVGEDFY-WIGLR 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 LGIKFPQVSSLVLEQQERLIQQDTALVNLTQWQRKYTLEYCQALLQRSLHSG-----SD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSPCPHNWIQNGKSCYYVFERWEMWNISKKSCLKEGASLFQIDSKEEMEFISSIGKLKGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKYWVGVFQ-DGISGSWFWEDGSSPLSDLLPAERQRSAGQICGYLKDSTLISDKCDSWKY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                          177 FISLKMIWIWVDGSPLDPKIFFIKGPAKENS----CAAIKESKIYSETCSSVFKWICQ 230
                                                                                                                                                                     DID---GWRWEDGPALSLSIL-----SNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Aorta, and Vein;
STRAIN=CS7BL/6J; TISSUE=Aorta, and Vein;
STRAIN=CS1SL/6B3; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Nature 420:563-573(2002).
SMBL; ARA041288; BAC30690.1; -.
MGD; MGI:2444608; 9830005566Rik.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001364; Lectin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LLYQRTLCCGSKGFMCSQ
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
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PRINTS; PR00356; ANTIFREEZEII.

SNART; SM00034; CIECT; 1.7

PROSITE; PSS0041; CIYPE_LECTIN 1; 1.7

PROSITE; PSS0041; CIYPE_LECTIN 2; 1.7

Hypothetical protein.

SEQUENCE 238 AA; 27014 MW; 0736BA0380B95EA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical C-type lectin domain containing protein.
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                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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                    57
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                     QBBRU4;
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RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 FSWMGLSDLNQEGTWQWYDGSPLSSSFQRYWNSGEPNNSGDEDCAEFSGSGWNDNRCNVD 407
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                       Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                               Bashirova A.A., Wu L., Cheng J., Martin T.D., Martin M.P., Benveniste R.B., Lifson J.D., KewalRamani V.N., Hughes A., Carrington M.; "Novel Member of the CD209 (DC-SIGN) Gene Family in Primates.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
SEQUENCE 422 AA; 48031 MW; 1F24460CBF991DC3 CRC64;
                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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MEDLINE=98124458; PubMed=9464811;
Vance R.E., Tanamachi D.M., Hanke T., Raulet D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.0%; Score 176.5; DB 6 29.9%; Pred. No. 2.5e-10; ive 19; Mismatches 57
  AA
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  422
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EMBL, AV078810; AAL89529:1; -
EMBL, AV078814; AAL89529:1; JOINED.
EMBL, AY078815; AAL89529:1; JOINED.
EMBL, AY078816; AAL89529:1; JOINED.
EMBL, AY078818; AAL89529:1; JOINED.
EMBL, AY078818; AAL89529:1; JOINED.
EMBL, AY078818; AAL89529:1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                         Created)
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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06,
25,
                                                      (TrEMBLrel. 23, (TrEMBLrel. 25,
                                     (TrEMBLrel. 23,
                                                                                                 Putative CD209L1 protein.
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PRELIMINARY;
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Best Local Similarity
Thes 38; Conserva
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408 NYWICKK 414
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             STRAIN=B1533;
PubMed=12477827;
                                                                                                                                                                                                   NCBI_TaxID=9590;
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                                                        01-MAR-2003
01-OCT-2003
                                       01-MAR-2003
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01-JUN-1998
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65 WYGHQCNCYFISKBEKSWERSRDFCASQNSSLLQ-PQSRNELSFWNF-SQTFFWIGMHYS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 SRWKVKAVLHR-PCVSYLVMVALGLLTVILMSLLLYQRTLC-CGSKGFM-CSQCSRCPNL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 RDIDGWRWEDGPALSLSILSN-SVVQKCGTIHRC-----GLHASSCEVALQWICEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 EKRNAWLWEDGTVPSKDLFPEFSVIRP----EHCIVYSPSKSVSAESCENKNRYICKKL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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TISSUE=Mammary gland;
Butcher S., Cottage A., Cook G.P.;
"Mouse natural killer cell receptors homologous to human CD94 and
"Cloning of a mouse homolog of CD94 extends the family of C-type lectins on murine natural killer cells.";

Bur. J. Immunol. 27:3236-3241(1997).

EMBL, AF030312; AAC8244.1;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Killer cell lectin-like receptor, subfamily D, member 1 (CD94)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 16.9%; Score 175; DB 11; Length 179; Similarity 27.9%; Pred. No. 1.3e-10; 50; Conservative 36; Mismatches 71; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                             MGD; MGT:119675; KITd1.

GO: GO:0005529; F:sugar binding; IEA.

InterPro; IPR001629; Ectin_C.

InterPro; IPR001804; Lectin_C.

PFam; PF00059; lectin_c; 1.

PROSITE; PS50041; CTYPE_LECTIN_2; 1.

PROSITE; PS00022; EGF 1; 1.

PROSITE; PS00022; EGF 1; 1.

SEQUENCE 179 AA; 20809 MW; D59EICBB63139E45 CRC64;
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Vance R.B., Tanamachi D.M., Hanke T., Raulet D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR006209; EGF_like.
InterPro; IPR001304; Lectin_C.
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SMART; SM00034; CLECT; l.
PROSITE; PS50041; C_TYPE_LECTIN_2; l.
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GO; GO:0005529; F:sugar binding; IEA
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65 WVCHQCNCYFISKEEKSWKRSRDFCASQNSSLLQ-PQSRNELSFMNF-SQTFFWIGMHYS 122
                                                                                                                                                                                                                                                                79 WMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL--- 135
                                                                                                                                                                                                     136 RDIDGWRWEDGPALSLSILSN-SVVQKCGTIHRC-----GLHASSCEVALQWICEKV 186
                                                                                                                                                                                                                                                                                                                                                                             123 EKRNAMIMEDGTVPSKDLFPEFSVIRP----EHCIVYSPSKSVSAESCENKNRYICKKI 177
                                                                                                                                                                            22 SRWKVKAVLHR-PCVSYLVMVALGLLTVILMSLLLYQRTLC-CGSKGFM-CSQCSRCPNL
                                                                                                                               22; Gaps
                                                                                        Length 179;
                                                                                                                               Indels
                                           179 AA; 20808 MW; DD343419E93B3465 CRC64;
                                                                                    Query Match 16.9%; Score 175; DB 11; Best Local Similarity 27.9%; Pred. No. 1.3e-10; Matches 50; Conservative 36; Mismatches 71;
PROSITE; PS00022; EGF_1; 1.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model protein search, OM protein August 10, 2004, 16:05:01; Search time 46.5841 Seconds (without alignments) 1140.281 Million cell updates/sec Run on:

US-09-811-367B-5 1036 score:

1 MADNSIYSTLELPAAPRVQD.....GLHASSCEVALQWICEKVLP 188 Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

A Geneseq_29Jan04:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		Aar77033 Mammalian	Aaw88277 Rat mast	Aae11761 Rat mast	Aae11760 Mouse ma	Aar77472 Partial	Add25635 Binding	Aaw88265 Human mas	_		Abj37898 NOVX prot	Humar	Aar54659 Human CD6	Aaw85593 Human CD6	Add25621 Binding	Aaw85594 Chicken	Aau02495 Human sec	Abj19328 NOVX rela	Abr43190 Human REM	Aae37769 Human C-t	Abb81897 Human NKp	Ade07884 Novel pro	Aau19657 Human nov	Abp47877 Human pol	σ.	
QI	1	AAR77033	AAW88277	AAE11761	AAE11760	AAR77472	ADD25635	AAW88265	AAE11759	ABG05451	ABJ37898	AAW88267	AAR54659	AAW85593	ADD25621	AAW85594	AAU02495	ABJ19328	ABR43190	AAE37769	ABB81897	ADE07884	AAU19657	ABP47877	ADC10839	
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Length 188; Indels

Query Match
100.0%; Score 1036; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.8e-96;
Matches 188; Conservative 0; Mismatches 0;

Sequence 188 AA;

Abr43189 Human REM Aay66765 Membrane— Aau12432 Human PRO Aab65288 Human PRO Abb43587 Membrane Abb43687 Human PRO Abu59103 Human PRO Abu17976 Novel hum Abu60612 Human sec Abu13994 Human PRO Abu13994 Human PRO Abu13994 Human PRO Abu13942 Human PRO Abu13942 Human PRO Abu66810 Human PRO Abu66810 Human PRO Abu66810 Human PRO Abu66810 Human PRO Abu59411 Novel Sec Abu59311 Novel sec	Human Human Human
ABR43189 AAY66765 AAU532 AAU532 AAB65288 ABB4358103 ABU59181 ABU59181 ABU13994 ABU13994 ABU13994 ABU813994 ABU813994 ABU813994 ABU813994 ABU813994 ABU813994 ABU813994 ABU813994	ABO25025 ABO25101 ABU59034
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ALIGNMENTS

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Mast cell function-associated antigen; MAPA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                      Mammalian mast cell function-associated antigen (MAFA).
                          AAR77033 standard; protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 37; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Tal M;
                                                                                                                                                                                                                                                                                                                         (YEDA ) YEDA RES & DEV CO LTD (RYCU/) RYCUS A.
                                                                                                                                                                                                                                                                      95WO-US004258.
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT01471
                                                                                                                                                                                       Rattus rattus.
                                                                                                                                                                                                                 WO9527734-A1.
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                                                                                                                                                                                                                                                                                               08-APR-1994;
                                                                             01-FEB-1996
                                                                                                                                                                                                                                          19-OCT-1995.
                                                                                                                                                          prevention.
                                                   AAR77033;
RESULT 1
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Gaps

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Length 188; Indels

Score 1036; DB 2; Pred. No. 1.8e-96; Mismatches 0;

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100.0%;

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CGGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120 121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180

61 61

MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN

1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL

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Query Match 100.
Best Local Similarity 100.
Matches 188; Conservative
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                                                                   CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFPDNQGVN 120
                                                                                           61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                          LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                          New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic
                                          09
                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of rat mast cell function-associated antigen (MARA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MARA molecule (see AAW88265) and to the discovery of splice variants (see AAW88266-67) of human MARA that are not found in rat. Polypeptides and synthetic of human MARA that are not found in rat. Polypeptides and synthetic and polynucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), and tumour growth
                                 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                               Mast cell function-associated antigen; MAFA; splice variant; rat; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                     Rat mast cell function-associated antigen (MAFA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32. .84
/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                              AAW88277 standard; protein; 188
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N-PSDB; AAV84222.
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Modified-site
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AAE11761 standard; protein; 188 AA.

WICEKVLP 188

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WICEKVLP

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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (MK) - or T-cell-expressed cell surface MAFA from binding to MAFA igand and a pharmaceutically acceptable excipient. The invention is cusful for inhibiting an NK- or T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition or to the subject, to NK or T-cell or the target cell ex; tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a cumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MAFA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
                                                                                                                                        antigen;
                                                                                                                                    Rat; pharmaceutical composition; mast cell function associated ant
MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell;
                                                                                                  Rat mast cell function associated antigen (MAFA) protein.
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                                                                                                                                                                                   immunosuppressive; cytostatic
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                                                           (first entry)
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                                                                                                                                                                                                                       Rattus norvegicus.
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                                                           18-DEC-2001
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                   AAE11761;
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Sequence 188 AA;

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Length 188; Indels

80.9%; Score 838; DB 4; 80.7%; Pred. No. 1.9e-76; iive 15; Mismatches 21

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to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface NAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is mouse MAFA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                     CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                          CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                               1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
                                                                                                                                                                                                                                                            1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 114 AA.
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                                                                                                                                                                                                                           Conservative
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Les 151, Conserv
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                                                                                                                                                      Sequence 188 AA;
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                                                                                                                                                                                                                                                                                                      LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                                                                                        CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse, pharmaceutical composition, mast cell function associated antigen, MAFA, natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
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                                                                                                                                                          MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLITVILMSLLLYQRTL
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                                                           Length 188;
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                                                           ), DB 4;
1.8e-96;
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                                                                                              0; Mismatches
                                                         100.0%; Score 1036; 100.0%; Pred. No. 1.
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64. .188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive; cytostatic.
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                                                                                              188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           WICEKVLP 188
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                                                                             Similarity
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                       Sequence 188
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                                                           Query Match
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Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
Partial sequence of mast cell function-associated antigen (MAFA).
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Length 114;

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immunoglobulin hinge region polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide. The CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human 1gG1 immunoglobulin hinge region polypeptide, a mutated human 1gG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human 1gG1 immunoglobulin hinge region polypeptide, where the first cysteine residues; where the first cysteine is not mutated; a mutated human 1gG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human 1gG1 immunoglobulin hinge region polypeptide derived from (a) having 3 or more cysteine residues; where the mutated human 1gG1 immunoglobulin hinge region polypeptide contains no more than one
                                                                                                                                                        75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
                                                                                                                                                                                                  CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a binding domain-immunoglobulin fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding domain; immunoglobulin; fusion protein; oytostatic; antiathritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; immunoglobulin heavy chain; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixa malipant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myaschenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding domain-immunoglobulin fusion protein-associated protein #95.
                                                                                                                                                                                                                                                 LRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVLP 188
                                                                                                                                                                                                                                                                           61 LRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVLP
                                                                                                                0; Indels
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                                                               62.8%; Score 651; DB 2; 100.0%; Pred. No. 8.1e-58; ive 0; Mismatches 0;
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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                                                                                                              Matches 114; Conservative
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                                                                                         Local Similarity
                     Sequence 114 AA;
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CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polymucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the polymucleotide (operabl) linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein or polymucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanowa, carcinowa or sarcoma, rheumatoid arthritis, subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanowa, carcinowa or sarcoma, rheumatoid arthritis, collections or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence the sequence. The printed specification and is also available in electronic format directly from USPTO at sequence the sequence. The present sequence is a binding domain-immunoglobulin the sequence the printed specification becapitated. The sequence the sequence in the printed specification becapited.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDDNQGVN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.7%; Score 545.5; DB 7 55.1%; Pred. No. 7.1e-47;
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/note= "Asn is N-glycosylated"
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/note= "ITIM motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of human mast cell function- associated antigen (WAFA), a type II membrane glycoprotein. CDNA (see AAV84198) encoding human MAFA can be obtained from myelogenous leukaemic cell line KUB12 or CDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW88277) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2 Alternatively spliced forms (see AAW8856-67) of human MAFA have been identified. Polypeptides and synthetic peptides (see AAW88258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and
                                                                                                                                                                                                                                                                                                             New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLITFPDNQGVN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLS-ILSNSVVQKCGTIHRCGLHASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, pharmaceutical composition, mast cell function associated antigen, MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human mast cell function associated antigen (MAFA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.7%; Score 525.5; DB 2; news...
61.5%; Pred. No. 7.4e-45;
                                                                                                                                                                                                                               Williams DH;
/note= "Asn is N-glycosylated"
150. .152
/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, and tumour growth
                                                                                                                                                                                                                               Lamont A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE11759 standard; protein; 189 AA.
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 44pp; English.
                                                                                                                                                                                               (PEPT-) PEPTIDE THERAPEUTICS LTD
                                                                                                                                98WO-GB001572
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                                                                                                                                                                                                                                                                                                                                                                diseases, and tumour growth.
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nes 100; Conservative
                                                                                                                                                                                                                               Lamers MBAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QWICEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HGVCKKV 187
                                                                                                                                                                                                                                                              WPI; 1999-059806/05.
                                                                                                                                                                                                                                                                                N-PSDB; AAV84198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 189 AA;
                Modified-site
                                                                  WO9854209-A2
                                                                                                                                29-MAY-1998;
                                                                                                                                                               31-MAY-1997;
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                                                                                                  03-DEC-1998
                                                                                                                                                                                                                               Hewitt EL,
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Matches
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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a traget cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition on the subject, to NK or T-cell or the target cell e.g. tumnour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating tumnour by simulating the cyclotxic activity of an NK cell or a cyclotxic T-cell (CTL), where the tumnour comprises an NK cell- or CTL-susceptible tumnour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is human MAFA protein
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53.5%; Pred. No. 7.4e-45;
iive 29; Mismatches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 18; 49pp; English.
                                                                                                                                                                                                         16-MAR-2001; 2001WO-US008596.
                                                                                                                                                                                                                                                                          17-MAR-2000; 2000US-0190716P.
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                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi N, Mikayama T;
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Best Local Similarity
Matches 100; Conserv
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                                                                WO200170805-A2
Homo sapiens
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Novel human diagnostic protein #5442.

(first entry)

22-MAY-2003

ABJ37898;

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reaction (PER) primers, oligomers, and for chromosome and gene with reaction (PER) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymolectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stees expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating in polypeptide and polymolectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Algonolo-AB030377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (II) are printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 QCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDF 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 BLPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMCS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          725 SCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLQVFLSEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YWIGLRDIDGWRWEDGPALSLSILSN-SVVQKCGTIHR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 35810; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
                                                                                                                                                                                                                                                                                 23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS69638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 843 AA;
                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
                                                                                     Homo sapiens.
                                                                                                                                                                       11-0CT-2001
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ABJ37898 standard; protein; 191 AA.

RESULT 10 ABJ37898 ID ABJ3

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anticonvulsant; antiaddictive; analgesic; dermatological; keratolytic; antiseborrheic; antirheumatic; antiarthritic; antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gusev V;
Boldog F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides, designated as NOVX, useful for diagnosing and treating infections, neurological diseases, cancer, allergy, and bone, immunological, skin, renal, brain, muscle and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rastelli L;
                                                                                                  Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer; vulnerary; virucide; antibacterial; protozoacide; fungicide; nootropic; antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
                                                                                                                                                                       cytostatic; antiasthmatic; antiporiatic; hypotensive; osteopathic; antiulcer; anorectic; antidabetic; antiallergic; haemostatic; antiulcer; anorectic; antidabetic; antiallergic; haemostatic; neuroleptic; antidepressant; antiinfertility; NOVX; human disease; NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal; paraaitic infection; Alzheimer's disease; stroke; forensic biology; immunogen; non-human transgenic animal; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhong M, Anderson D, Ballinger R, Gerlach V, Spytek KA, Rastel Kekuda R, Guo X, Zerhusen B, Andrew D, Mezes P, Patturajan M; Burgess CE, Eisen A, Wolenc A, Baungartner J, Shimkets RA, Gus Vernet CAM, Taupier RJ, Pena C, Shenoy S, Li L, Casman S, Bol Fernandes E, Smithson G, Malyankar U, Taillon B, Liu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tchernev V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decristofaro MF, Padigaru M, Miller C,
                                                                       NOVX protein sequence SEQ ID No 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 118; 672pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0277388P
2001US-0278151P
2001US-0278857P
2001US-0285140P
2001US-0285141P
2001US-0297444P
2001US-0297444P
2001US-0297444P
2001US-02960P
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2001US-0275990P.
2001US-0276449P.
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2001US-0263799P.
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2001US-0272870P.
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2001US-0304886P.
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2001US-0264139P.
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2001US-0312937P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-058504/05.
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                                                                                                                                                                                                                                                                                                            WO200281517-A2
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20-APR-2001;
20-APR-2001;
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20-MAR-2001;
23-MAR-2001;
                                                                                                                                                                                                                                                                                Unidentified.
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09-AUG-2001;
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08-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-2001;
24-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                         17-0CT-2002
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cell function-associated antigen; MAFA; huMAFA(E3/4-);

Mast

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polypeptide and polymucleotide, by measuring the level of polypeptide expression or the amount of mucleic acid from a mammal and comparing it with another mammal not having or not predisposed to the disease. Novx polypeptide is also useful for identifying an agent that binds to Novx polypeptide is also useful for identifying an agent that binds to Novx mad a cell expressing Novx is useful for identifying an agent that both that both as the expression or activity of Novx. The antibodies and a polypeptide having 95 % sequence identify to Novx polypeptide are useful for determining the presence or amount of Novx in a sample. Novx polypeptides are useful for treating a pathological state in a mammal. The antibodies are also useful for determining the presence or amount of Novx in a sample. Novx polypeptides are useful for treating or preventing disorders or syndromes including trauma, viral, bacterial, fungal, processing an agarastic infections. They can also treat disorders such as e.g., Alzheimer's infections. They can also treat disorders such as e.g., Alzheimer's disease or a stroke. The Novx encoding nucleic acids are useful for expressing the Novx proteins, to detect. Novx many, or a genetic lesion in a NovX gene and to modulate Novx activity. NovX sequences are also useful for instruction and to modulate Novx activity. NovX sequences are also useful for use in identifying a cell or tissue type in a biological sample, to amplify has or an indentifying and/or cloning NovX homology and as primers and probes the nor and probes in other cell
                             (NOVI - 33), consisting of a mature form of one of 61 sequences, given in variant differation, or its variant, where amino acid residue(s) in the variant differ from the mature form, provided that the variant differs in not more than 15 % of the amino acids from the sequence of the mature form one more than 15 % of the amino acids from the sequence of the mature form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and an antibody to the polypeptides, are useful for treating or preventing a NOVX-associated disorder in humans and for treating a syndrome associated the encoding nucleic acids, are useful for determining the presence of or predisposition to a disease sosciated with altered levels of NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. The NOVX nucleic acids can be used in gene therapy. This sequence represents a NOVX protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     types. The NOVX proteins are useful as an immunogen to generate antibodies which are useful for diagnostically monitoring protein levels and modulating NOVX activity. Cells comprising NOVX nucleic acids are
       designated NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for producing non-human transgenic animals which are useful for
invention relates to a novel isolated polypeptide,
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129 DFYWIGLRDIDGWRWE-----DGPAL--SLSILSNSVVQKCGTIHRCGLHASSCEVAL 179 72 CKICEPCPTSWLPFGGSCYYFSVPKTTWAEAQGHCADASAHLAAFPEDRKVAFYSVLLGR 131 132 CLFGIGLARVGGWRWQVAPGTQIDAPAVGQGACFCQESI-----SGLPASELRLEK 182 LPAAPRVQDDSRWKVKAVL--HRPCVSY-LVMVALGLLTVILMSLLLYQRTLCCGSKGFM 68 CSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE Gaps 21; DB 6; Length 191; Indels 84; ; Score 251.5; DB 6; Pred. No. 3.8e-17; 24; Mismatches 84 24.3%; 31.4%; 59; Conservative 183 WWHCSKTL 190 180 QWICEKUL 187 Query Match Best Local Similarity Sequence 191 AA; 12 69 12 Matches à 8 qq d à ð à

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Human MAFA splice variant huMAFA(E3/4-).
        AAW88267 standard; protein; 99 AA.
                                         (first entry)
                                         29-MAR-1999
                        AAW88267
AAW88267
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New polypeptide having a sequence corresponding to human mast cell function associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated MAFA polypeptides including huMAFA(E3/4-), and polynuclectides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-17), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ISSNSFVQTCGAITKNGLQASSCEVPLH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of human mast cell function- associated antison (MARA) splice variant huMARA(E334-), which lacks the C-lectin-like domain of human MARA (see AAWM82265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MIDSVIYSMLELPTATQAQNDYGPQQKSSSSRPSCSCLVAIALGLLTAVLLSVLLYQWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immune system; thrombocyte development; signal transduction; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                human; inflammation; allergy; asthma;
                                                                                                                                                                                                                                                    Williams DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.0%; Score 207.5; DB 2 29.6%; Pred. No. 4.7e-13; iive 12; Mismatches 30
              splice variant; human; inflammation; a rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                      Lamont A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR54659 standard; protein; 199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3; 44pp; English.
                                                                                                                                                                                                                     (PEPT-) PEPTIDE THERAPEUTICS LTD
                                                                                                                                                         98WO-GB001572
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                                                                                                                                                                                                                                                      Lamers MBAC,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                    N-PSDB; AAV84200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 99 AA;
                                                              Homo sapiens.
                                                                                           WO9854209-A2.
                                                                                                                                                        29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ---
                                                                                                                                                                                                                                                    Hewitt EL,
                                                                                                                          03-DEC-1998
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(INCY-) INCYTE PHARM INC.
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N-PSDB; AAV83109.
                                                                                                                                                                 Shah P;
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les 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 199 AA;
                                       29-APR-1998;
                                                                                29-APR-1997;
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05-NOV-1998
                                                                                                                                                                 Bandman O,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of human CD69. The CD69 protein is active in the regulation and function of the immune system. The protein may be used for blocking thymocyte development in in vitro systems. The soluble polypeptide can be used to competitively bind the ligand in vivo thus inhibiting signal transduction activity via endogenous cell surface bound CD69. CD69 may also be used to generate antibodies. See also AAR54660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG--WRWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 VMNVVFITILIIALIALSVGQYN---CPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFIST 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lectin, carbohydrate; binding; agglutination; selectin; receptor;
calcium dependent binding; treatment; cancer; detection; identification;
CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD69 nucleic acids and polypeptide - used in the diagnosis, therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 VSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMC---SQCSRCPNLWMRNGSHCYYFSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    study of the activation and regulation of the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "soluble polypeptide"
                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW85593 standard; protein; 199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 27; 35pp; English.
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26.3%;
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assay; diagnosis; therapy
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                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP.
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N-PSDB; AAQ65340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 199 AA;
                                       Homo sapiens
                                                                                                                                                                                                                                               28-OCT-1993;
                                                                                                                                                                                                                                                                                         29-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                              Ziegler SR,
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                                                                                                    Protein
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Recombinant cells contraining expression vectors comprising the CTL-1 conding sequence can be used to produce recombinant CTL-1 which is useful for raising Ab and to screen for specific binding agents Binding agents which are antagonists of CTL-1 can be used to treat or prevent cancer, e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are used to diagnose these conditions, as probes or primers in usual hybridisation and/or amplification assays, or for gene mapping, while complements of this sequence, antisense or ribozyme sequences are used to treat or prevent the aforementioned cancers also. Ab are used directly as antagonists or for delivery of therapeutic agents to cells that express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding domain; immunoglobulin; fusion protein; cytostatic; antiatrhritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; GH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-fisorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 VMNVVFITILIIALIALIALSVGQYN---CPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFIST 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG--WRWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 VKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVGLKKEPGHPWKWSNGKEF 161
                                                                                                                                                                                                                                                                                                                                                                                       New human C-type lectin and related nucleic acid, vectors, transformed cells - antibodies, agonists and antagonists, for diagnosis, prevention and treatment of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 VSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFMC---SQCSRCPNLWMRNGSHCYYFSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding domain-immunoglobulin fusion protein-associated protein #88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) also a transmembrane domain, but no secretory signal. CTL-1 also shomology with chicken 17.5.3 (AAW85594), and mouse CD69 (AAW85595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD69 shows homology with the human CTL-1 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 N-NWFNVTGSDKCVFLKNTEVSSMECEKNLYWICNK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.8%; Score 184.5; DB 2
26.3%; Pred. No. 2.4e-10;
ive 30; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD25621 standard; protein; 199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 48; 64pp; English.
98WO-US008791
                                                                      97US-00846523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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4;

92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG--WRWEDGPAL 149

102 VKRSWISAQNACSEHGAILAVIDSEKDMNFIKRYAGREEHWVGLKKKEPGHPWKWSNGKEF 161

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150 SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185

AAW85594 standard; protein; 257 AA

RESULT 15 AAW85594 (first entry)

(revised)

17-0CT-2003 02-MAR-1999

AAW85594;

Chicken 17.5.3 protein.

lectin, carbohydrate; binding; agglutination; selectin; receptor; calcium dependent binding; treatment; cancer; detection; identification; CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.

Gallus gallus

WO9849306-A1

05-NOV-1998.

97US-00846523.

29-APR-1997;

29-APR-1998;

σ

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New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell
                                                                                                                                      subject having or suspected of having a malignant condition or disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                     Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
                                                                                                                                                          Disclosure; SEQ ID NO 182; 157pp; English
                                                           17-JAN-2001; 2001US-0367358P.
17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                              25-JUL-2002; 2002US-00207655
                                                                                      (GENE-) GENECRAFT INC
                                                                                                                  WPI; 2003-801317/75.
                   US2003118592-A1.
      Unidentified.
                                 26-JUN-2003
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The Invention transfer to a binding domain-lumunoglobulin tusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, and immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the CH2 constant region polypeptide. and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine is not mutated, a mutated human IgG1 immunoglobulin hinge region polypeptide derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains contains a cysteine region polypeptide contains of the mutated human IgG1 immunoglobulin hinge region polypeptide derived from (a) having 3 or more cysteine residues, and a mutated human IgG1 immunoglobulin hinge region polypeptide contains of cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains of cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains of cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibod. Construct comprising the polymucleotide (operably linked to a promocer), a not cell transformed or transfected with a recombinant expression construct comprising the polymucleotide (operably linked to a promocer), a host cell transformed or transfected with a recombinant expression construct comprising the bolymucleotide (operably linked to a promocer), a host cell transformed or transfected with a recombinant expression construct comprising the bolymucleotide (operable) is respected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is subject having subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, mysthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease the present sequence is a binding domain sequence data for this patent formed part of the printed specification and is also available in electronic formet directly from uSprO at sequence. huml?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified. The invention relates to a binding domain-immunoglobulin fusion protein Sequence 199 AA;

Example 3; Page 48-49; 64pp; English. homology with human CD69 (AAW85593) New human C-type lectin and cells - antibodies, agonists and treatment of cancers. Sequence 257 AA; 4 9. 17.8%; Score 184.5; DB 7; Length 199; 26.3%; Pred. No. 2.4e-10; 76; Indels 30; Mismatches

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Chicken 17.5.3 protein shows homology with the human CTL-1 protein.
Recombinant cells containing expression vectors comprising the CTL-1
coding sequence can be used to produce recombinant CTL-1 which is useful
coding sequence can be used to produce recombinant CTL-1 which is useful
coding sequence can be used to produce recombinant CTL-1 which is useful
cofficiently, paraganglion, penis, brain, thyroid and heart which are
ssociated with overexpression of CTL-1. Fragments of this sequence are
used to diagnose these conditions, as probes or primers in usual
hybridisation and/or amplification assays, or for gene mapping, while
complements of this sequence, antisense or ribozyme sequences are used to
treat or prevent the aforementioned cancers also. As are used directly as
antagonists or for delivery of therapeutic agents to cells that express
CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) and
construction the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the constr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vectors, transformed diagnosis, prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nomology with human CD69 (AAW85593), and mouse CD69 (AAW85595) proteins (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctin and related nucleic acid, agonists and antagonists, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 99
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28.6%; Pred. No. 3.7e-10;
cive 23; Mismatches 66
(INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Conservative
                                                                                                                                                                                                                                                                      WPI; 1999-024060/02.
                                                                                                                                      Shah P;
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV83109
                                                                                                                                      Bandman O,
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August 10, 2004, 16:18:53; Search time 40.2619 Seconds (without alignments) 1464.718 Million cell updates/sec
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1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188
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| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1291235 seqs, 313682936 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d \			SUMMARIES	
Result	Č	Query	:			
. ON	Score	Match	Match Length DB	DB	ID	Description
1	1036	100.0	188	σ	US-09-811-367B-5	Segmence 5. Appli
7	838	80.9	188	δ	US-09-811-367B-3	Sequence 3. Appli
3	545.5	52.7	189	14	US-10-207-655-196	Semience 196. Ann
4	525.5	50.7	189	6	US-09-811-367B-1	Sequence 1. Appli
S	184.5	17.8	199	10	US-09-284-320-86	Segmence 86. April
9	184.5	17.8	199	14	US-10-207-655-182	Segmence 182. App
7	184.5	17.8	199	14	US-10-179-528-3	Spinor & apromoted
80	184.5	17.8	199	15	US-10-379-127-26	Luck 30 Apro-
Q	184	17.8	257	14	US-10-179-528-4	Segmence 4. Appli
10	182	17.6	268	15	US-10-161-493-22	Segmence 22. April
11	180	17.4	231	16	US-10-451-843-1	Semience 1 Appli
12	179.5	17.3	265	σ	US-09-764-870-307	Semience 307 App
13	179.5	17.3	265	14	US-10-125-540-307	Semience 307 Ann
14	179.5	17.3	275	15	US-10-161-493-20	Semience 20 April
15	177.5	17.1	229	9	US-09-989-722-424	

4 0.44444

Sequence 424, App		424	424	424	424	424	424	424,	424	424,	424,	424,	424,	424	424,	424	424,	424,	424	424	424	424	424	424	424	424	424	424	42
9 US-09-989-723-4	9 US-09-989-279-4	-60-SD 6	-60-SD 6	٠.	-60-SD 6	-60-SD 6	σ	9-866-60-SD 6	066-60-SD 6	-60-SD 6	-60-SN 6	9 US-09-989-2	9 US-09-989-735-4	٠.	•	229 9 US-09-989-730-424	229 9 US-09-990-436-424	6-60-SD 6	10 US-0	10 US-09-	10 US-09-993-6	10 US-09-997-428	10 US-09-997-666-4	10 US-09	10 US-	10 US-09-	10 US-09-	10 US-09-	229 10 US-09-990-437-424
5.	177.5	177.5	177.5	177.5 1	177.5 1	177.5 1	3 177.5 1	177.5	5 177.5 1	6 177.5 1	7 177.5 1	177.5	177.5	0 177.5 1	1 177.5 1	177.5 1	33 177.5 17.1	177.5 1	5 177.5 1		7 177.5 17.	8 177.5 1	9 177.5 17.	0 177.5 17.	177.5 17.	177.5 17.	177.5 17.	.5	H

ALIGNMENTS

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APPLICANT: GEMINI SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifumi
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
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; Pred. No. 2.7e-99;
0; Mismatches 0;
                                                                                                                                                                                      FILE REFERENCE: 021286/0278719
CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                  ; Sequence 5, Application US/09811367B; Patent No. US20020155110A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 188; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Rattus norvegicus
                                                              GENERAL INFORMATION:
US-09-811-367B-5
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Sequence 1, Application US/09811367B

Sequence 1, Application US/09811367B

GENERAL INFORMATION:
APPLICANT: GENINI SCIENCE, INC.
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
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US-09-284-320-86
Sequence 86, Application US/09284320
Publication No. US20030092175A1
GENERAL INFORMATION:
APPLICANT: KACO, Seishi et al.
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
TITLE OF INVENTION: ENCODING THESE PROTEINS
FILE REPREBNCE: GIM-6705CPUS
CURRENT APPLICATION NUMBER: US/09/284,320
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: UF 8-301429
9
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1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 021286/0278719
CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
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181 HWVCKKV 187
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US-09-811-367B-1
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Sequence 3, Application US/09811367B
Patent No. US20020155110A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takahashi, No. US20020155110A1uaki
APPLICANT: Takahashi, No. US20020155110A1uaki
APPLICANT: MIKAyama, Toshifumi
ITILE OF INVENTION: SOLUBLE MAST
TITLE OF INVENTION: SOLUBLE MAST
TITLE OF INVENTION: SOLUBLE MAST
TITLE OF INVENTION: US 1200201319
CURRENT PAPLICATION NUMBER: 60/190,716
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ 1D NOS: 20
SOFTWARE: PatentIn version 3.0
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APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 3900694.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT APPLICATION NUMBER: US/10/207,655
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
TYPE: PRT
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Best Local Similarity 55.1%; Pred. No. 2.3e-48;
Matches 103; Conservative 28; Mismatches 55;
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80.7%; Pred. No. 9.7e-79;
iive 15; Mismatches 21,
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Publication No. US20030118592A1
GENERAL INFORMATION:
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Best Local Similarity 80.7%
Matches 151; Conservative
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US-10-207-655-196
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                                                                     181 WICEKVLP 188
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                             WICEKVLP
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US-09-811-367B-3
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                                                                                                                                                                                                                                                                                                                                                               EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG--WRWEDGPAL 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 182, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TILLE REPERENCE: 390069.401C1
CURRENT APPLICATION UNMER: US/10/207,655
UNMERO PER SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 182
                                                                                                                                                                                                    Length 199;
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26.3%; Pred. No. 7.2e-11;
""" """ """ """ "" Tabels
                                                                                                                                                                                               17.8%; Score 184.5; DB 10; Length
26.3%; Pred. No. 7.2e-11;
tive 30; Mismatches 76; Indels
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TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                               150 SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                       162 N-NWFNVTGSDKCVFLKNTEVSSMECEKNLYWICNK 196
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PRIOR FILING DATE: 1996-11-13
PRIOR APPLICATION NUMBER: PCT/JP97/04056
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 91
SCOFTWARE: Patentin Ver. 2.0
SEQ ID NO 86
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Publication No. US20030166136A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                    41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                           ORGANISM: Homo sapiens
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Best Local Similarity
Matches 41; Conserva
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Best Local Similarity
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                                                                                                         LENGTH: 199
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                                                                                                                            TYPE: PRT
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APPLICANT: Entage, Peter C.R.
APPLICANT: Entage, Radoje
APPLICANT: Demanac, Radoje
APPLICANT: Goodrich, Ryle
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TAR
TITLE OF INVENTION: OF CELLS THAT EXPRESS DCAL-HY POLYPEPTIDES
TITLE OF INVENTION: OF CELLS THAT EXPRESS DCAL-HY POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/379,127
CURRENT APPLICATION NUMBER: US 09/799,451
PRIOR PRILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 VKRSWISAQNACSEHGATLAVIDSEKDMNFLKRYAGREBHWYGLKKEPGHPWKWSNGKEF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 VMNVVFITILIALIALSVGQYN---CPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFIST 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 VSYLVMVALGLLTVILMSLLLLYQRTLCCGSKGFMC---SQCSRCPNLWMRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                               CURRENT APPLICATION:
CORRUPTER: TBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASTEEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,528
FILING DATE: 24-0un-2002
CLASSIFICATION ATMORPM: US/846,523
FILING DATE: CURROWN-
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/846,523
FILING DATE: CURROWN-
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 N-NWFNVTGSDKCVFLKNTEVSSMECEKNLYWICHK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                      ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 26, Application US/10379127; Publication No. US20040005592A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                               MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                   \mathbf{USA}
                                                                                                                             COUNTRY: US
ZIP: 94304
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                                                                                                       STATE: CA
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Page

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45 VMNVVFITILIALIALSVGQYN---CPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFIST 101
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                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                          DB 15; Length 199;
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OPERATING SYSTEM: DOS
OPERATIOR SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,528
FILING DATE: 24-Jun.2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shah, Purvi
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          Query Match 17.8%; Score 184.5; DB 15; Best Local Similarity 26.3%; Pred. No. 7.2e-11; Matches 41; Conservative 30; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
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APPLICATION NUMBER: US/08/846,523
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10179528
Publication No. US20030166136A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 257 amino acids
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MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SOFTWARE: PatentIn version 3.1
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                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-379-127-26
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                                   SEQ ID NO 26
LENGTH: 199
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US-10-179-528-4
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DB 14; Length 257;

Score 184;

17.8%;

Query Match

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IITLE OF INVENTION: No. US20040018555A1el Antibodies that Bind to Antigenic Polypept
IITLE OF INVENTION: Acids Encoding the Antigens, and Methods of Use
                    9
                                                                                                        101 PC-----MLVLALVAVIVL-----ORPSCSPRPPF----SHVCPNAWVGFQGKCYYFSDT 146
                                                                                                                                                  93 KRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG----WRWEDGPAL 149
                                                                                                                                                                                         147 ESDWNSSREHCHRIGASLATLDTKEEMEFMLOYORPADRWIGLHRAEGDEHWTWADGSAF 206
                                                             33 PCVSYLVMVALGLITVILMSLILYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSME 92
                      26; Gaps
                      Indels
                                                                                                                                                                                                                                      150 SLSILSNSVVQ-----KCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                 T----NRPVFELRGGGRCAYLNGDGISSALCHSEKFWVCSR 243
28.6%; Pred. No. 1.1e-10;
ive 23; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/161,493
CURRENT FILING DATE: 2002-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION UNBER: 60/337,524
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-66-06
PRIOR FILING DATE: 2001-66-06
PRIOR PELING DATE: 2001-66-06
PRIOR APPLICATION NUMBER: 60/296,575
PRIOR APPLICATION NUMBER: 60/296,575
PRIOR APPLICATION NUMBER: 60/297,151
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2001-66-17
PRIOR FILING DATE: 2001-66-17
PRIOR FILING DATE: 2001-66-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-06-12
APPLICATION NUMBER: 60/341,143
FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/337,524
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/10161493
Publication No. US20040018555A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taupier Jr., Raymond J
Guo, Xiaojia Sasha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boldog, Ferenc L
Malyankar, Uriel M
Padigaru, Muralidhara
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Gerlach, Valerie
Shimkets, Richard A
Gorman, Linda
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Smithson, Glennda
Bdinger, Shlomit R
Millet, Isabelle
Ellerman, Karen
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MacDougall, John R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patturajan, Meera
Spytek, Kimberly A
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Shenoy, Suresh G
Hialt, Tord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zerhusen, Bryan D
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Anderson, David W
  Best Local Similarity 28.6
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leite, Mario W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Voss, Edward Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pena, Carol EA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhong, Mei
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 PNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNL----FQEYVGEDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 WIGIRDIDG----WRWEDGPALSLSIL----SNSVVQKCGTIHRCGLHASSCEVALQWIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 LGVKLLQVSTIAMQQQEKLIQQERALLNFTEWKRSCALQMKYCQAFMQNSLSSAHNSSPC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---QCSRC 75
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           62;
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                                                                                                                                                                                                                                                                                                                                                  17.3%; Score 179.5; DB 9; Length 265; 26.4%; Pred. No. 3.4e-10; live 29; Mismatches 84; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 307, Application US/10125540
Publication No. US20030059875A1
GENERAL INFORMATION:
FULL TROUGH et al.
TITLE OF INVENTION:
CURRENT APPLICATION:
CURRENT APPLICATION Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION Number: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
ERNOTH: 265
                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nacleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------CCGSKGFMCS--
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                                                                                                                                                                                                                                                                                                                                                                                           84;
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                             Sequence 307, Application US/09764870
Patent No. US20020042386A1
GENERAL INFORMATION:
                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 307
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 64; Conserv
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Best Local Similarity
Matches 64; Conserv
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           JS-09-764-870-307
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Publication No. US20040115738A1
GENERAL INFORMATION:
APPLICANT: INNATE PHARMA S.A.S.
APPLICANT: UNIVERSITA DI GENOVA
TITLE OF INVENTION: Polypeptides having a triggering NK receptor activity and biologi
FILE REFERENCE: 1249NKP80
                                                                                                                                                                                                                                                            71 QCSRCPNLWMRNGSHCYYFSM-EKRDWNSSLKFCADKGSHLLTFP--DNQGVNLFQEYVG 127
                                                                                                                                                                                                                                                                                    128 EDFYWIGLR-DIDG--WRWEDGPALSLSILSNSVVQK-----CGTIHRCGLHASSCEVA 178
                                                                                                                                                                                                                                                                                                                                                              Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:|:|:|
51 LTLTLISLIL---LVSCGVLLKCQKG-SCSNATQYEDTGDLKVNNGTRRNISNKDLCASR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 E-DFYWIGLRDID----GWRWEDGPALSLSIL-----SNSVVQXCGTIHRCGLHASSCE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::|||| :::|||
167 QLNYUWIGLNFTSLKMTWTWDGSPIDSKIFFIKGPAKENS----CAAIKESKIFSETCS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----YLVMVAL-----GL
                 PRIOR FILING DATE: 2001-06-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 299
                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
                                                                                                                                                                                            Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                    Score 182; DB 15;
Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 180; DB 16;
; Pred. No. 2.5e-10;
38; Mismatches 74;
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                                                                                                                                                                         17.6%; Scor.
31.5%; Pred. No. ...
'''a 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/451,843
CUMRENT FILING DATE: 2003-12-30
CUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VERSION 3.1
PRIOR APPLICATION NUMBER: 60/297,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.4%;
21.8%;
                                                                                                                                                                                                                         40; Conservative
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                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-451-843-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     : |||||
251 IFWICEK 257
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                             US-10-161-493-22
                                                                       SEQ ID NO 22
LENGTH: 268
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Best Local S:
Matches 54
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67 FMCSQCSRCPNLWMRNGSHCYYFSM-EKRDWNSSLKFCADKGSHLLTFP--DNQGVNLFQ 123
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhang, Zemin
TITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC63
                                                                                                                                                                                                                            11; Gaps
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 299
SEQ ID NO 20
                                                                                                                                                                                    Length 275;
                                                                                                                                                                                 17.3%; Score 179.5; DB 15; Length
31.5%; Pred. No. 3.5e-10;
ive 22; Mismatches 56; Indels
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CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR PLILNG DATE: 1997-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 424, Application US/09989722 Patent No. US20020072067A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kljavin, Ivar J.
                                                                                                                                                                                                                                 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 EVALOWICEK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eaton, Dan L.
                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-161-493-20
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                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 41; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-989-722-424
                                                                                 LENGTH: 275
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APPLICANT:
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APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Hillet, Isabelle
APPLICANT: Hillet, Isabelle
APPLICANT: Blerman, Karen
TITES OF INVENTION: Acids Encoding the Antigens, and Methods of Use
FILE REFERENCE: 21402-377A
CURRENT APPLICATION NUMBER: 60/295,607
FRIOR APPLICATION NUMBER: 60/295,607
PRIOR PRING DATE: 2001-06-06
PRIOR PRING DATE: 2001-06-06
PRIOR PRILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/296,575
PRIOR FILING DATE: 2001-06-11
PRIOR FILING DATE: 2001-06-11
PRIOR FILING DATE: 2001-06-11
PRIOR FILING DATE: 2001-06-11
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
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PRIOR FILING DATE: 2001-06-12
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PRIOR FILING DATE: 2001-06-12
                                                                                                                                                      76 PNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNL----FQEYVGEDFY 131
                                                                                                                           WIGLEDIDG----WRWEDGPALSISIL----SNSVVQKCGTIHRCGLHASSCEVALQWIC
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FILING DATE: 2001-12-14
APPLICATION NUMBER: 60/297,567
FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taupler Jr., Raymond J
Guo, Xiaojia Sasha
Miller, Charles E
Shenoy, Suresh G
Hjalt, Tord
Voss, Edward Z
                                                                                                                                                                                                                                                                                                                               RESULT 14

US-10-161-493-20

; Sequence 20, Application US/10161493

; Publication No. US20040018555A1

; GRWERAL INFORMATION:

; APPLICANT: Anderson, David W

· APPLICANT: Zernisen, Bryan D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boldog, Ferenc L
Malyankar, Uriel M
Padigaru, Muralidhara
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Casman, Stacie J
Gerlach, Valerie
Shimkete, Richard A
Gorman, Linda
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Spytek, Kimberly A
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MacDougall, John R
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NUMBER: 60/083322 1988-04-28 NUMBER: 60/084600 1998-05-07 NUMBER: 60/087106 1998-05-28 NUMBER: 60/087607 1998-06-02 1998-06-02 1998-06-02 1998-06-02 NUMBER: 60/08769 1998-06-04 1998-06-04 1998-06-04 1998-06-04 1998-06-04	06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-04 06-05 06	06-09 1 60/08873 1 60/08873 1 60/08874 1 60/08881 1 60/08882 1 60/08882 1 60/08882 1 60/08882 1 60/08885 1 60/08885 1 60/08885 1 60/08885 1 60/08885 1 60/08885	99 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
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                                                                                                                                                                                       Query Match
17.1%; Score 177.5; DB 9; Length 229;
Best Local Similarity 26.9%; Pred. No. 4.5e-10;
Matches 61; Conservative 32; Mismatches 83; Indels 51;
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1980-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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Search completed: August 10, 2004, 16:32:38 Job time : 41.2619 secs

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Sequence 2, 1 Sequence 17, Sequence 31, Sequence 12,

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Run on:

Sequence:

Searched:

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Score 1036; DB 3; Length 188;
Pred. No. 1.3e-105;
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Patent No. 6034227
GENERAL INFORMATION:
PECHT, ISTAEL
APPLICANT: BECHT, ISTAEL
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: D.C.

COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/US95/04258
FILING DATE: 06-APR-1995
RICH APPLICATION DATA:
APPLICATION NUMBER: 11 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWNY, ROGET L.
REGISSMALION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1A
TELECOMMUNICATION INFORMATION:
THE EDUNICATION INFORMATION:
US-08-650-095-9

US-08-650-578-2

US-08-650-578-2

US-09-113-788-3

US-09-113-789-9

PCT-US93-10418-4

US-09-517-605-2

US-08-772-440-10

US-08-772-440-12

US-08-772-440-31

US-08-772-946-12

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US-09-111-470-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
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    TOPOLOGY: linear
MOLECULE TYPE: protein
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Database :

No. Result

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75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                             1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
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                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: GUTHANN, Marcelo D.
APPLICANT: GTHANN, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: DE FC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION NUMBER: IS 10,109257
APPLICATION NUMBER: IS 10,109257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.8%; Score 651; DB 3; I
Best Local Similarity 100.0%; Pred. No. 9.7e-64;
Matches 114; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington STATE: D.C. COUNTRY: UNTTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.C. : UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                            RESULT 3
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Parent No. 6034227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFRENCE/DOCKET NUMBER: PECH
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 amino acids
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MOLECULE TYPE: protein
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STRANDEDNESS: si
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PCT-US95-04258-6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING STEM: COMPATIBLE
SOFTWARE: PATENTIN BATH:
CURRENT APPLICATION DATH:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRICK DATE: 08-APR-1994
ATTCRNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELECHONE: 202-628-5197
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAFA) NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESS
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TYPE: amino acid
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                      Conservative
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                      Matches 188;
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                                                                                                                         3 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG
                                                      Gaps
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    Query Match 26.4%; Score 273; DB 4; Length 76; Best Local Similarity 59.7%; Pred. No. 1.4e-22; Matches 43; Conservative 14; Mismatches 15; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.8%; Score 184.5; DB 5; 26.3%; Pred. No. 2.4e-12; tive 30; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                          PCT-US93-10418-2
; Sequence 2, Application PC/TUS9310418
; Sequence 2, Application:
    GENERAL INFORMATION:
    APPLICANT: Ziegler, Steven F.
    APPLICANT: Hjerrild, Kathryn A.
    TITLE OF INVENTION:
    NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 2610-WO IBLECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 13, Application US/08772440 ; Patent No. 6046158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 587-04:
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                       RESULT 6
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US-09-531-056A-23

Sequence 23, Application US/09531056A

Patent No. 6455683

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: DAM MOLECULES. ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: DB20 NP OWDER: US/09/531,056A

CURRENT APPLICATION UNDER: US/09/531,056A

CURRENT FILING DATE: 2000-03-20

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin version 3.0

SEQ ID NO S33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPNIMMRNGSHCYYFSMEKRDWNSSIKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 LRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVLP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVLP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                  A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.8%; Score 651; DB 5; I
100.0%; Pred. No. 9.7e-64;
iive 0; Mismatches 0;
                                                                                                           NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PECHT=1 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
Application PC/TUS9504258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 114, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
PCT-US95-04258-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23
                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
Sequence 6, Applicati
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                     CITY: Washingt
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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Sequence 6, Application US/09531056A;
Patent No. 6455683
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: D820 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT APPLING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 CSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFYWIGLRDIDG--WRWEDG------PALSLSILSNSVVQKCGTIHRCGLHASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YLQDENENRIGILQQLAKRFCQYVVKQSELKGTFKGHKCSPCDINWRYYGDSCYGFFRHN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MADNSIYSTLEL----PAAPRVQDDSR--WKVKA-VLHRPCVSYLV-MVALGLLTVILMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MODEDGYITLNIKTRRRALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 LLLYQRTLCCGS------KG-FMCSQCSRCPNLWMRNGSHCYYFSMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 RDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFY---WIGL---RDIDGWRWEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLL--LYQRTLCCGSKGFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 191;
                                                                                                                                                                                                                                                                                                                                                      Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 ALSISILSNSVVQ-----KCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 ----SVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCER 218
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.8%; Score 174.5; DB 4
25.8%; Pred. No. 2.8e-11;
iive 29; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                          Score 175.5; DB 4
Pred. No. 2.8e-11;
                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Conservative
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.9%
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 48; Conserv
                                                                                                                                              SOFTWARE: Patent.pm
SEQ ID NO 97
LENGTH: 229
                                                                                                                                                                                                                                                                NAME/KEY: SIGNAL LOCATION: -47..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-531-056A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-531-056A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                 APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: THEREOF
NUMBER OP SEQUENCES: 42
CORRESPONDENCE ADDRES:
ADDRESSEE: ALTOId, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 TLCCGSKGFMCSQCSRCPNIMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 VNLFQEYVGE---DFYWIGL--RDIDG-WRWEDGPA------LSLSILSNSVVQKCGTI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 FSTQDIHKRPRGSEKGSRAPSSPW-----RP----IAVGLGILCFVVVVVAAVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YSTLELPAAPRVQD-----DSRWKVKAVLHRPCVSYLVMVALGLL--TVILMSLLLYQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.9%; Score 175.5; DB 3; Leugen. 26.2%; Pred. No. 2.3e-11;
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEMIN PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT FILING DAIE: 1999-02-09
BARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DAIE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 HRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 HGSEVYNQICNTSSYSICEKEL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 97, Application US/09247155A Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFRERNCE/DOCKET NUMBER: UTXD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.2
Matches 53, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-772-440-13
        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-247-155-97
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                     CITY: Madison
STATE: New Jes
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                         07940
                                                                                                                       ADDRESSEE:
STREET: On
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-07587-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-722-126A-8
                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AAPR-VQDDSRWKVKAVLHRPC--VSYLVMVALGLL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RCPNLWMRNGSHCYYF 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 DGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.4%; Score 169.5; DB 2; Length : 26.1%; Pred. No. 1.2e-10; ive 32; Mismatches 84; Indels
                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Chang, Chiwen
APPLICANT: Chang, Chiwen
APPLICANT: Lanier, Levis L.
APPLICANT: Lanier, Levis L.
APPLICANT: Phillips UT., Joseph H.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,435
FILING DATE: 16-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0397
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 TVILMSLLLYQRTLCCGSKGFMCSQCS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,462
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              Sequence 2, Application US/08738462
Patent No. 5965401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 225 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                     :||| |
181 KWICSK 186
180 QWICEK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE
                                                                                                   US-08-738-462-2
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RESULT 11 PCT-US94-07587-2

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59 SVSVTSLI--QKS-----SIEKCSVDIQQSRNKTTERPGLLNCPIYWQQLREKCLLF 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 DGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
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Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: BECHT, Israel
APPLICANT: TAL, Michael
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MARA)
Sequence 2, Application PC/TUS9407587
GENERAL INFORMATION:
APPLICANT: Schering Corp.
TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND
TITLE OF INVENTION: RELATED REAGENTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 TVILMSLLLYQRTLCCGSKGFMCSQCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: DX0397K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7255
TELEPAX: 201-822-7039
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07587
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
                                                                                                                                                                                            E: Schering Corp.
One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MADNSIYSTLELP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                   New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                16.1%; Score 166.5; DB 5; 27.4%; Pred. No. 1.1e-10; trive 22; Mismatches 57;
                                                                   PECHT=1 PCT
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FILING DATE: 15-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,717
FILING DATE: 29-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,430
FILING DATE: 01-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 31-JUL-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/089,168
FILING DATE: 12-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/127,946
FILING DATE: 31-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US 60/069,692
16-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09127946
Patent No. 6416973
                     NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECH'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             115 amino acids
                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acid
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-8
                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.1%; Score 166.5; DB 3; Length 115; Best Local Similarity 27.4%; Pred. No. 1.1e-10; Matches 31; Conservative 22; Mismatches 57; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                   CURRENT APPLICATION DATA:

SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/722,126A
FILING DATE: 09-0CT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWN, ROGET L.

NEGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MA
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN
TITLE OF SEQUENCES: 10
CORRESSED ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY Mashington
STATE: D.C.
    D.C. : UNITED STATES OF AMERICA
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 115 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-722-126A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                            20004
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                         COUNTRY:
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75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDDNQGVNLFQEYVGEDFYWIG 134
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                                                                                                                                                                                                                                                  61 LKKEPGHPWKWSNGKEFN-NWFNVTGSDKCVFLKNTEVSSMECEKNLYWICNK 112
                                                  3;
Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bakker, Alexander B.H.
APPLICANT: Phillips, Joseph H.
APPLICANT: Phillips, Joseph H.
APPLICANT: Indier, Lewis L.
TITLE OF INVENTION: Mammalian Cell Membrane Proteins;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES:
AUMBER OF SEQUENCES:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GEDFYWIGLRDIDG---WRWEDGPALSLSILSNSVVQKCGTIHRCGL----HASSCEVAL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 16.1%; Score 166.5; DB 4; Length 190; l Similarity 24.3%; Pred. No. 2.1e-10; 45; Conservative 31; Mismatches 66; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Ford, John
APPLICANT: Saeland, Sem
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
TITLE OF INVENTION: Related Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 MVALGLLTVIL-----MSLLLYQRTLCCGSKGFMCSQC-
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APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-UUL-1997
ATYORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: S4,090
REFERENCE/DOCKET NUMBER: SF0695
TELECOMMUNICATION INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET WIMBER: DX0763X
TELECOMMUNICATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/111,470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OFTWARE: PATENCE.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-127-946-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palo Alto
: California
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182 RWICE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 QWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1104
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STATE: Califor
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-111-470-10
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Best Local 8
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75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
                                                                                                                                                                                                                                                                                                         ---KCGTIHRCG-LHASSCEVAL 179
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                           15;
                                                                                                                                                                                               Query Match 15.9%; Score 164.5; DB 3; Length 273; Best Local Similarity 27.2%; Pred. No. 5.6e-10; Matches 34; Conservative 19; Mismatches 57; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: August 10, 2004, 16:20:32 Job time : 15.6407 secs
                                                                                                                                                                                                                                                                                                                                                           135 LRDIDG-WRWEDGPALSLSILSNSVVQ-
(650)852-9196
            TELBFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          180 QWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 HWVČE 262
  TELEPHONE:
                                                                                             TYPE: amin
TOPOLOGY:
                                                                                                                                           ; MOLECULE 1114
US-09-111-470-10
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Colden) Albola export silly

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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model using sw protein search, protein ĕ

August 10, 2004, 16:30:38; Search time 17 Seconds Run on:

(without alignments) 1069.423 Million cell updates/sec

US-09-811-367B-1 Title: Perfect score:

1023 1 MIDSVIYSMLELPTATQAQN.....GLQASSCEVPLHGVCKKVRL 189 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues

Searched:

95820 Total number of hits satisfying chosen parameters:

length: 0 length: 189 sed Minimum DB s Maximum DB s

100% Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

aggretin beta chai pancreatic thread pancreatic stone p pancreatitis-assoc lectin BRA3-2 prec coagulation factor echicetin beta cha bitiscetin alpha c pancreatic stone pregenerating prote hepatic lectin hom natural killer cel aggretin alpha cha pancreatitis-assoc pancreatic stone p botrocetin alpha c lectin BRA3-1 prec pancreatitis-assoc coagulation factor coagulation factor bitiscetin beta ch perlucin - Halioti mast cell function agkisacutacin beta antifreeze protein regenerating islet botrocetin beta ch regenerating islet C type lectin, B Description SUMMARIES WMVZF2 T28140 PC7027 JC7135 S29825 A28351 A28351 A28351 A34313 A34313 A41719 A4 JC2415 JC5058 JC4329 B42972 JC5059 S78774 854979 B47267 RGHUIA 159421 LNRC1 Query Match Length DB 12.0 12.5 12.7 12.7 12.5 12.1 12.0 11.9 11.7 166 153.5 149 143.5 142 137.5 136 135 134.5 132.5 130.5 129.5 128 128 123.5 122.5 122 121.5 120 119.5 118.5 118.5 Score Result Ño.

reg II, regenerati	reg I, regeneratin	agkisacutacin alph	echinoidin - sea u	hepatic lectin hom	coagulation factor	pancreatitis-assoc	lectin - barnacle	ovocleidin - chick	A40R protein - vac	SalF2R protein pre	NK cell_receptor h	hypothetical prote	type II antifreeze	hypothetical prote	hypothetical prote
347148	A47148	JC7134	A26697	WMVZF8	JC4690	A48689	S10548	378596	F42521	7777	T37425	T26692	JC7938	T33623	T25730
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2	7	2	7	Н	N	Н	7	N	N	N	7	Ŋ	N	N	N
173 2 1	165 2	152 2	147 2	116 1	152 2	174 1	173 2	142 2	168 2	159 2	168 2	158 2	147 2	188 2	173 2
	•			10.3 116 1	•		• •		•						•
10.8	10.8	10.6	10.3		10.3	10.1	6.6	8.6	8.6	9.7	9.7	9.7	6.9		8.7

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	9421	
B	4	
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mast cell function associated antigen - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 02-201-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 C;Accession: I59421 R;Guthmann, M.D.; Tal, M.; Pecht, I. Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995 A;Title: A secretion inhibitory signal transduction molecule on mast cells is another C A;Reference number: I59421; MUID:96016176; PMID:7568140 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-188 <RES>

A;Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142 C;Genetics:

A; Gene: mafa

; ; Length 188; Indels 51.4%; Score 525.5; DB 2; llarity 53.5%; Pred. No. 4.8e-42; Conservative 29; Mismatches 57; Local Similarity es 100; Conserv Query Match Best Loca Matches

120 61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS ò

61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120 d

121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180 ŏ В

181 HGVCKKV 187 ð

QWICEKV 186

RESULT 2
128141
C type lectin, B locus - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T28141
R; Milne, S.; Kauffman, v.; Beck, S.
submitted to the EMBL Data Library, May 1998
A; Description: DNA sequencing and analysis of the chicken major histocompatibility comp

A;Accession: T28141 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

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Occidentacin beta chain precursor - sharp-nosed viper
NyAlternate names: fibrinogenlytic venom protein
('jepecies Agristrodon acutus (sharp-nosed viper)
('jepecies Agristrodon acutus (sharp-nosed viper)
('joaces Agristrodon acutus (sharp-nosed viper)
('joaces Agristrodon acutus (sharp-nosed viper)
('joaces Agristrodon acutus (sharp-nosed viper)
('joacession: JC7135; Pc7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A,Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic veno A,Feefence number: JC7134; MUID:20025379; PMID:10558903
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: man agrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggretin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet
A;Reference number: PC7027; MVID:99443731; PMID:10512747
A;Accession: PC7027
A;Accession: PC7027
A;Residues: 1-144 <CHU>
A;Residues: 1-144 <CHU>
A;Residues: 1-144 <CHU>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                     2
                 A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
A;Experimental source: clone cB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARD--SHILVITDNQEMSLLQVF 125
                                                                                                                                                                                                                                                                                                                                          70 ASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
                                                                                                                                                                                                                                                                                                                                                                                               45 AACILICPQFWRILIGDRCYBLSTEKGNWTQAKMKCENLQSQLAVLRKKAEEDHLQQMAGAE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 PVWIGLEVSTNOWKWVDNSSYNSTESDNLSVMENRCGTFKNTKVEGDVCSGEHQWVCQK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 FCWIGLR-NNSGWRWEDGSPLNFSRISSNSFVQT-CGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 TRAGLEDCDFGWSPYDQHCYQAFNEQKTWDEAEKFCRAQENGAHLASIESNGEADFVSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 LS-----EAFCWIGLR----NNSGWRWEDGSPLNFSRISSNSFVQTCGAINK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 144;
                                                                                                                                                                                                                       ch 14.6%; Score 149; DB 2; Length 17
1 Similarity 28.6%; Pred. No. 9.9e-07;
34; Conservative 16; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                             A;Map position: 16
A;Note: Intron positions not resolved (incomplete sequence)
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A;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 143.5; DB 2
29.6%; Pred. No. 2.7e-06;
iive 17; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 34; Conserv
  A; Residues: 1-170 <MIL>
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                                                                                                                  A; Gene: B-NK
                                                                                        C, Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatic lectin homolog (BamHI-ORF2) - fowlpox virus (isolate HP-438 [Munich])

C;Species: fowlpox virus

C;Species: fowlpox virus

C;Species: fowlpox virus

C;Species: fowlpox virus

C;Date: 30-8ep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000

C;Accession: B29663

R;Tomley, F; Binns, M.; Campbell, J.; Boursnell, M.

J; Gen. Virol. 69, 1022-1040, 1988

A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox

A;Reference number: JT0442; MUID:88229622; PMID:2836548

A;Recension: B29663

A;Rocession: B29663

A;Rocession: B29663

A;Rose-references: GB:D00295; NID:9221380; PIDN:BAA00192.1; PID:9221383

C;Reywords: early protein

F;49-152/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         natural killer cell receptor homolog - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T28140

R;Milne, S.; Kaufman, J.; Beck, S.

Submitted to the EMBL Data Library, May 1998

A;Description: DNA sequencing and analysis of the chicken major histocompatibility compl

A;Reference number: Z20475

A;Accession: T28140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
A;Residues: 1-156 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A;Experimental source: clone cB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 FCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGLRNNS---GWRWEDGSPLNFSRISSNS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SHL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRIS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
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                                                                                                                                                                                                                                                                                                                                                                          42 TLGLLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%; Score 153.5; DB 1; Length 167; 25.8%; Pred. No. 3.7e-07; tive 29; Mismatches 74; Indels 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 NCSALGASLAVFDSAEDLSFTMRHKGSSPHWVGLSREGKEHPWEWVNRSPL-
                                                                                                                                                                                                                             Length 156;
                                                                                                                                                                                                                                                                                     68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F-VQ---TCGAINKNGLQASSCEVPLHGVCKKVRL 189
                                                                                                                                                                                                                             16.2%; Score 166; DB 2;
29.7%; Pred. No. 2.3e-08;
iive 19; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 SNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
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                                                                                                                                                                                                                                                                                  46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Conservative
                                                                                                          A,Gene: BLec
A,Map position: 16
A,Introns: 17/1; 74/3; 110/2
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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Matches
                                                                                        Genetics;
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Db ð qq ò dd

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Aintrons: 21/1; 60/3; 106/3; 144/1
C;Superfamily: tetranectin; C-type lectin homology
C;Rewords: pyroglutamic acid
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-165/Product: pancreatic stone protein #status predicted <MAT>
F;35-161/Domain: C-type lectin homology <LCH>
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Note: parts of this sequence, including the amino end of the mature protein, were detrally the amino end of the mature protein is blocked
A.Note: the amino end of the mature protein is blocked
B.Ng, N.F.; Trinh, K.Y.; Hew, C.L.
J. Biol. Chem. 261, 15690-15652, 1986
A.Title: Structure of an antifreeze polypeptide precursor from the sea raven, Hemitripting A.Reference number: A24602; MUID:87057207; PMID:3782083
                                                                                                                                                                                                                                R;Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovery, M. Comp. Biochem. Physiol. B 93, 793-797, 1989
A;Title: Characterization in rat pancreatic juice of a protein homologous to the human A;Reference number: PLO147; MUID:90031455; PMID:2680252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Comment: This protein is found in pancreatic calculi of mammals. A peptide bond betwe rotein into an insoluble protein at a neutral pH of 5.5 to 7.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antifreeze protein II precursor - sea raven
NyAlternate names: pro-antifreeze protein type II
SyBecdes: Hemitripterus americanus (sea raven)
CyBecdes: Hemitripterus americanus (sea raven)
CyBecdes: 10-Sep-1999
#sequence revision 10-Sep-1999 #text_change 10-Sep-1999
CyAccession: A34313; A24602; PC2386; PC2387; S65733
R.Hayes, P.H.; Scott, G.K.; Ng, N.F.L.; Hew, C.L.; Davies, P.L.
J. Biol. Chem. 264, 18761-18767, 1989
A.Title: Cystine-rich type II antifreeze protein precursor is initiated from the third and the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the c
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A; Residues: 22-69 < ADR>
A; Residues: 22-69 < ADR>
A; Experimental source as
A; Experimental source as
B; Dusetti, N.J; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.
Biochim. Biophys. Acta 1174, 99-102, 1993
A; Title: Rapid PCR cloning and sequence determination of the rat lithostathine gene.
A; Reference number: S34618; MUID: 93326645; PMID: 7916640
                                                                                                                                                                                              A;Cross-references: GB:M62930; GB:J05722; NID:g206462; PIDN:AAA41974.1; PID:g206463
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A; Molecule type: DNA; mRNA
A; Residues: 1-37, 'G', 39-163 < HAY>
A; Residues: 1-37, 'G', 39-163 < HAY>
A; Cross-references: GB: J05100; NID: g213875; PIDN: AAA49618.1; PID: g213876
A; Note: there are 12-15 copies in the genome; the sequence of SR7 was determined A; Note: the initiator codon was determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 VLLSVLLYQWILCQGSNYSTCASCPS----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 NWNSGYLVSVLSQAEGNFLASLIKESGTTAANVWIGLHDPKNNRRWHWSSGSLFLYKSWD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 ILLSCLM---VLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSWAEADLFCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 ARDS-HLLVITDNQEMSLLQVFLSE----AFCWIGL---RNNSGWRWEDGSPLNF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-165 <DUS>
A;Cross-references: EMBL:L07512; NID:g393208; PIDN:AAA41533.1; PID:g393209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 SRISSNSFVQTCGAINKNG----LQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 TGYPNNSNRGYCVSVTSNSGYKKWRDNSCDAQLSFVCK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.4%; Score 137; DB 2; 27.2%; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Mismatches
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Best Local Similarity 27.28
Matches 43; Conservative
                                                                                                                                             1-165 <ROU>
                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                          preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
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A,Molecule type: mRNA
A;Residues: 1-165 <TER>
A;Residues: 1-165 <TER>
A;Cross-references: GB:M18962; NID:g206604; PIDN:AAA42028.1; PID:g206605
A;Cross-references: GB:M18962; NID:g206604; PIDN:AAA42028.1; PID:g206605
B;Rouquier, S: Verdier, J.M.; Iovamna, J.; Dagorn, J.C.; Giorgi, D.
J. Biol. Chem. 266, 786-791, 1991
A;Title: Rat pancreatic stone protein messenger RNA. Abundant expression in mature exoct A;Reference number: A39081; MUID:91093273; PMID:1985964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1172, 184-186, 1993
A;Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homolog
A;Reference number: S29821; MUID:93176807; PMID:7679928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NyAlternate names: lithostathine
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: Al-Mar-1990 #sequence revision) 31-Mar-1990 #text_change 11-May-2000
(Species: Al-May-1990 #sequence revision) 4.7 Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamot R; Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamot A; Biol. Chem. 257, 2111-2114, 1988
A;Title: A novel gene activated in regenerating islets.
A;Reference number: A92704; MUID:88115343; PMID:2963000
                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 SLEFCLA--RDSHLLVITDNOE----MSLLQVFLSEAFCWIGLR---NNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AEKFCTOOHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKWSDGTKL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 FSVEEKDWNSSLEFCLAR-DSHLLVITDNQEMSLLQVFL----SEAFCWIGLR----- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 IPQIPQTWFDAELACQKRPGGHLVSVLNSAEASFLSSMVKRTGNSYQYTWIGLHDPTLGA 113
                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                         5 IFVSFGLLVVFL-------SLSGTAADCPSEWSSYEGHCYKPFDEPKTWAD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPTACSV-----MSWMLLSCLM---LLSQVQGEDSLKNIPSARISCPKGSQAYGSYCYA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 BPNGGGWEWSNNDVMNYFNWERNPSTALDRAFCGSLSRASGFLKWRDMTCEVKLPYVCK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 --NNSGWRWEDGSPLNFSRISSNSFVQT----CGAINK-NGL---QASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Mus musculus [house mouse]
                                                                                                                                                                                                                                                                                      39 VAITLGLLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 PSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYSTCASCP----SCPDRWMKYGNHCYY
                                                                                                                                                                                              Gaps
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F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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                                                                                                 Length 146;
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; Pred. No. 1.2e-05;
28; Mismatches 70;
                                                                                                 ; DB 2; I
3.9e-06;
                                                                                                                                                                                         21; Mismatches
                                                                                                 Score 142;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreatitis-associated protein - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Dec-1993 #sequence revision 1
                                                                                                 13.9%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 13.4%;
l Similarity 25.7%;
46; Conservative 2
                                                                                                                                                                                              42; Conservative
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: S29822
R; Itoh, T.; Teraoka, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-175 <ITO>
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A;Status: preliminary
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                                                                                            Query Match
Best Local S
Matches 42
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A41719

AA1719

PANOTECATIC Stone protein 2 precursor - rat

PANOTECATIC Stone protein 2 precursor - rat

C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A37456; A5313; II51899; UC1257; A41719
C;Date: 16-Oct.1992 #sequence revision 16-Oct.1992 #text_change 20-Jun-2000
C;Date: 16-Oct.1992 #sequence revision 16-Oct.1992 #text_change 20-Jun-2000
C;Date: 16-Oct.1992 #sequence revision 16-Oct.1992 #text_change 20-Jun-2000
C;Date: 16-Oct.1992 #sequence revision 16-Oct.1992 #text_change 20-Jun-2000
C;Date: 16-Oct.1992 #sequence revision 16-Oct.1993
A;Title: Structural organization of the gene encoding the rat pancreatitis-associated p
A;Reference number: A37456; MUID:9330847; PMID:8314803
A;Reciule type: DNA
A;Residues: 1-175 cDUS.
A;Residues: 1-175 cDUS.
A;Residues: 1-175 cDUS.
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A;Residues: 1-175 cDUS.
A;Residues: 1-175 cDUS.
A;Residues: 1-1859333
A;Reciules: 1-1859333
A;Reciules: 1-1953
A;Reciules: 1-1953
A;Re
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J. Clin. Invest. 86, 1004-1013, 1990
A;Title: Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease
A;Reference number: A37194; MUID:90368981; PMID:2394826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 38-138/44-175 <CAI>
A,Residues: 38-138/44-175 <CAI>
C,Comment: The purified protein undergoes a reversible globule-fibril transformation of C,Comment: The purified protein homology
C,Keywords: disulfide bond; extracellular protein; pancreas
F;38-138/Product: pancreatic thread protein chain A #status experimental <ACH>
F;40-171/Domain: C-type lectin homology <LCH>
F;41-175/Product: pancreatic thread protein chain B #status experimental <BCH>
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49 AERFCKLQPKHSHLVSFQSAEEADFVVKLTRPRLKANLVWMGLSNIWHGCNWQWSDGARL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Species: Bos primigenius taurus (cattle)
C,Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
C,Accession: A37194; A53897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 TLGL--LTAVLLSVLLYQWILCQGSNYSTCASCP----SCPDRWMKYGNHCXYFSVEEXD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 WMDADIACOKRPSGHLVSVLSGAEESFVASLVRNNLNTQSDIWIGLHDPTEGSEANAGGW
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A)Molecule type: mRNA
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                                                                                                                                                                   150 NFSRISSNSFVQTCGAINKNGLQ---ASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic thread protein precursor - bovine
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F.35-163/Product: antifreeze protein II #status predicted <MAT>
F.35-163/Product: antifreeze protein II #status predicted <MAT>
F.34-159/Domain: C-type lectin homology <LCH>
F.35/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F:41-52,69-159,135-151/Disulfide bonds: #status predicted
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C; Species: Calloselasma rhodostoma (Malayan pit viper)
C; Species: Calloselasma rhodostoma (Malayan pit viper)
C; Accession: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C; Accession: U77105
R; Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A; Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet A; Reference number: PC7027; MUID:99443731; PMID:10512747
A; Rocession: U77105
A; Molecule type: mRNA
A; Residues: 1-146 < CHU>
A; Residues: 1-146 < CHU>
A; Residues: 1-146 < CHU>
C; Superfamily: tetranectin; C-type lectin homology
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: disulfide bond; platelet aggregation; venom
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                                                                         A,Residues: 'MORGADDEREDISTAGLSIIFIVCTISTIR',1-163 <NGN>
A,Residues: 'MORGADDEREDISTAGLSIIFIVCTISTIR',1-163 <NGN>
A,Residues: 'MORGADDEREDISTAGLSIIFIVCTISTIR',1-163 <NGN>
A,Rotes: parts of this sequence were determined by protein sequencing
A,Boucker, B.P., Gauthier, S.Y., Davies, P.L.
Biochem. Biophys. Res. Commun. 203, 1851-1857, 1994
A,Title: Cystine-rich fish antifreeze is produced as an active proprotein precursor:
A,Reference number: PC2386; MUID:95032070; PMID:7945337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 18-27 < NUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-37 CNUZ-316, 1996
Biochim. Biophys. Acta 1292, 312-316, 1996
A; Title: Bridence for a proprotein intermediate during m A; Reference number: 865733; MUID:96176860; PMID:8597578
A; Accession: 865733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Keywords: pyroglutamic acid
F;1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ajintrons: 21/1; 66/3; 105/3; 142/1
C;Superfamily: tetranectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 İĞGSACLQAGAWTWSDĞTPMNF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 IG---LRNNSGWRWEDGSPLNF 151
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A,Residues: 18-22 <DUW>
C,Genetics:
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Best Local Similarity
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A;Residues: 1-45 <DUN>
A;Accession: PC2387
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R;Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Vern.
Eur. J. Biochem. 224, 29-38, 1994
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J. Clin. Invest. 90, 2284-2291, 1992
J. Clin. Invest. 90, 2284-2291, 1992
J. Clin. Invest. 90, 2284-2291, 1993
J. Clin. Invest. 90, 2284-2291, 1993
A; Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in A; Reference number: I55580; MUID:93107309; PMID:1469087
A; Accession: I55580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Structural organization and chromosomal localization of a human gene (HIP/PAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 KSWTDADLACOKRPSGNLVSVLSGAEGSFVSSLVKSIGNSYSYVWIGLHDPTOGTEPNGE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -CPDRWMKYGNHCYYFSVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: hepatocellular carcinoma
A;Note: sequence extracted from NCBI backbone (NCBIN:113007, NCBIP:113008)
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C;Superfamily: tetranectin; C-type lectin homology
C;Reywords: acute phase; extracellular protein; pancreas
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-175/Product: pancreatitis-associated protein #status predicted <MAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-171/LH-146-163/Disulfide bonds: #status predicted
                                                                                                                                            A,Cross-references: GB:L15533; NID:g482908; PIDN:AAA60020.1; PID:g482909 R,Lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C. Cancer Res. 52, 5089-5095, 1992
A,Title: A novel gene (HIP) activated in human primary liver cancer. A,Reference number: A44931; MUID:92386513; PMID:1325291
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-175 <LAS>
A;Cross-references: GB:X68641; NID:g312806; PIDN:CAA48605.1; PID:g312807
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A;Title: Cloning and tissue-specific expression of CDNAs
A;Reference number: S29821, MID:93176807; PMID:7679928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S48197; MUID: 94357229; PMID: 8076648
A; Accession: S48197
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Matches 46; Conservative
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                                                        A;Molecule type: DNA
A;Residues: 1-175 <DUS>
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A;Residues: 1-175 <LA2>
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A; Residues: 1-175 <RES>
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A; Statules; preliminary; ranslated irom GB/EMBL/DDBU
A; Molecule type: mRNA
A; Kesidues: 1-175 <10V1>
A; Cross-references: GB:M98049; NID:g393210; PIDN:AAA16341.1; PID:g393211
A; Mote: in Gembank entry RATPARC, release 113.0, the source is designated as Rattus ratt R; Mote: in Gembank entry RATPARC, release 113.0, the source is designated as Rattus ratt R; Mote: in Gembank entry Accession. JG1257
A; Molecule type: mRNA
A; Reference number: JG1257; MUID:92380521; PMID:1511905
A; Molecule type: mRNA
A; Residues: 1-6, 'S', 8-175 <KAM>
A; Molecule type: mRNA
A; Residues: 1-6, 'S', 8-175 <KAM>
A; Cross-references: GB:S33715; NID:g254694; PIDN:AAB23103.1; PID:g254695
B; Covanna, J'; Orelle, B.; Keim, V'; Dagorn, J.C.
J Biol. Chem. 266, 24664-24669, 1991
A; Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein, a A; Molecule type: mRNA
A; Residues: 1-175 < CLOV2>
A; Cross-references: GB:M55149; NID:g206030; PIDN:AAA41807.1; PID:g206031
A; Molecule type: mRNA
A; Residues: 1-175 < CLOV2>
A; Cross-references: GB:M55149; NID:g206030; PIDN:AAA41807.1; PID:g206031
A; Molecule type: mRNA
A; Residues: 1-175 < CLOV2>
A; Cross-references: GB:M55149; NID:g206030; PIDN:AAA41807.1; PID:g206031
A; Molecule type: mRNA
A; Residues: 1-175 < CLOV2>
A; Molecule the amino-terminal residue of the mature protein was identified as Glu
C; Genetics: Ray
A; Molecule type: MRNA
A; Molecule type: MRNA
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pancreatitis-associated protein precursor - human
NyAlternate names: C-type lectin; pancreatic stone protein homolog HIP
NyAlternate names: C-type lectin; pancreatic stone protein homolog HIP
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 21-Jul-2000
C;Accession: A46915; Z53821; S48197; I55580
R;Dusetti, N.J.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.
Genomics 19, 108-114, 1994
A;Title: Molecular cloning, genomic organization, and chromosomal localization of the hu
A;Reference number: A49616; MUID:94245143; PMID:8188210
A,Reference number: A59313
A,Accession: A59313
A,Accession: A59313
A,Accession: A59313
A,Status: not compared with conceptual translation
A,Molecule type: DNA
A,Residues: 'MMRVK',1-175 <DUS2>
A,Cross-references: GB:L07127; NID:g349550; PIDN:AAA41805.1; PID:g349551
A,Cross-references: GB:L07127; NID:g349550; PIDN:AAA41805.1; PID:g349551
A,Note: an incorrect initiation codon was used
R;Iovanna, J.L; Keim, V.; Bosshard, A.; Orelle, B.; Frigerio, J.M.; Dusetti, N.; Dagorn
Am. J. Physiol. 265, G611-G618, 1993
A;Title: PAP, a pancreatic secretory protein induced during acute pancreatitis, is expre
A,Reference number: I51899; MUID:94056762; PMID:8238345
A,Reference number: I51899
A,Status: preliminary; translated from GB/EMBL/DDBJ
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F1.27-175/Product: pancreatitis-associated protein #status experimental <MAT>
F1.27-175/Product: pencreatitis-associated protein #status experimental <MAT>
F1.40-171/Domain: C-type lectin homology <LCH>
F1.40-51,68-171,146-163/Disulfide bonds: #status predicted
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les 42; Conserv
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Search completed: August 10, 2004, 16:35:20 Job time : 18 secs
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Best Local
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                                                                                                  Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure an
A;Reference number: JC1503; MUID:9329294; PMID:8514190
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A;Reference number: JC4329; MUID:96318509; PMID:8749314
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R; Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A; Title: The primary structure of coagulation factor IX/factor X-binding protein isolate otein, tetranectin, and lymphocyte Rc epsilon receptor for immunoglobulin E.
A; Reference number: A39332; MUID:91332000; PMID:1831197
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 25-162 < MUR>
A; Residues: 25-162 < MUR>
A; Note: 146-Arg was also found
C; Comment: This three galactose-binding lectin is isolated from the coelomic fluid.
C; Comment: The protein plays important roles in defense mechanisms and in development C; Comment: The molecule is a terramer of identical chains.
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: hemolymph; homotetramer; lectin
F; 1-24/Domain: signal sequence #stane productions.
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                             ;Accession: JC1504; A26094
;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba,
                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-162 cTAK>
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A;Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
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A;Cross-references: DDBJ:DB3332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
31-Dec-1988 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
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F;25-162/Product: lectin BRA3-2 #status experimental <AMT>
F;25-150/Domain: C-type lectin homology <LGH>
F;26-150/LS5-142/Disulfide bonds: #status experimental
F;26-39,56-150,125-142/Disulfide bonds: #status experimental
F;157/Disulfide bonds: interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental
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A;Residues: 24-146 <ATO>
R;Atoda, H: 1shikawa, M: Yoshihara, E.; Sekiya, F.; Morita,
T. Biochem. 118, 965-973, 1995
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25.5%; Pred. No. 6.4e-05;
Live 26; Mismatches 56
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77 LAFQTFGHSIF-WMGLSNVWNQCNWQWSNAAMLRYKAWAEESYCVYFKSTN-NKWRSRAC 134
A; Accession: JC4330
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 24.146 <AT2>
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: anticoagulant; blood coagulation; lectin; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: factor IX/X binding protein chain B #status predicted <MAT>
F;25-142/Domain: C-type lectin homology <LGH>
F;25-142/Domain: C-type lectin homology <LGH>
F;25-36,53-142,119-134/Disulfide bonds: #status predicted
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nes 32; Conservative
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O93426
P42854
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P81996 |
P81112
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                           141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAP1_HUMAN
LEC3_MEGRO
IXB_TRIFL
LITB_HUMAN
RHCA_AGKRH
ABA4_TRIAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOTA_BOTJA
ABAL_TRIAB
PLC_HALLA
CVXA_CRODU
PAP3_RAT
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V239 FOWPV
V008 FOWPV
PBCG MESAU
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LITH_RAT
ANP_HEMAM
LITH_BOVIN
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MMHB AGKHA
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Maximum Match 100%
Listing first 45 summaries
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                                                              using sw model
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Gapop 10.0 , Gapext 0.5
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CHBB_
                                                                                                                                                              US-09-811-367B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein search,
                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 189
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137.5
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129.5
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                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                           Searched:
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Perfect :
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	P21063	VA40 VACCC	Н	168	8.6	100.5	45
gallus gall	Q9prs8	OC17_CHICK	r-i	142	9.6	100.5	44
	P35231	PAP2_RAT	Н	174	10.1	103	43
trimeresuru	P23806	IXA_TRIFL	Н	152	10.3	105	42
anthocidari	P06027	LECE_ANTCR	H	147	10.3	105.5	41
homo sapien	043908	NKGF_HUMAN	Н	158	10.4	106.5	40
agkistrodon	69Y999	MMHA AGKHA	Н	157	10.7	109	39
mus musculu	P43137	LIT1_MOUSE	Н	1.65	10.8	110	38
mus musculu	Q08731	LIT2 MOUSE	Н	173	10.8	110.5	37
trimeresuru	P81115	ABBA TRIAB	Н	132	10.9	111.5	36
sus scrofa	029191	LITH_PIG	Н	122	11.0	112.5	35
trimeresuru	P81113	ABA3 TRIAB	Н	125	11.0	113	34

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21158386; PubMed=11261935;
Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
Ksavitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rheasts monkey decidua.";
Immunogenetics 53:69-73(2001).
                                                                                                                                                                                                                                                                                                                                                                                                         ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

MEDLINE=20322487; PubMed=10866118;
LaBonte M.L., Levy D.B., Letvin N.L.;
Lacker, C.P., Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B,
                                                    OWAZE, USGK91, Q9MZK7; Q9MZK8; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1).
                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyms=CD94-B; Isold=Q9MXK9-2; Sequence=VSP_003055; Name=3; Synonyms=CD94 alt; Isold=Q9MXK9-3; Sequence=VSP_003054; Isold=Q9MXK9-3; Sequence=VSP_01564; -: TISSUE SPECIFICITY: Natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
IsoId=Q9MZK9-1; Sequence=Displayed;
                                          179 AA
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 [mmunogenetics 51:496-499(2000)
                                                                                                                                                                                 KLRD1 OR CD94.
Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF190931; AAF74527.1; -. EMBL; AF190932; AAF74528.1; -.
                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
NCBL_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               members
                                          CD94_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                              and D."
RESULT 1
CD94 MACMU
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EMBL; AB009597; BAA24450.1; --
EMBL; AB010084; BAA24451.1; --
EMBL; BC028009; AAH28009.1; --
PDB; 1B6E; 15-UUN-99.
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  136
                                                                                                                                                                                                                                                                                                                                                                                             93 EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                          78
                            InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SWART; SM00034; CLECT; 1.
PROSITE; PS060515; CTYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; Polymorphism.
                                                                                                                                                                                                          N-LINKED (GLCNAC. ..) (POTENTIAL).
MAVEKTTLWRLISGTLGIICLSLMATLGIILLKNS -> MAA
                                                                                                                                                                                                                                                                                                                                                                                                          | | | | | | | :: | | | :: | | | | EKTWNESRHFCASQKSSLLQLQNRDELDFMS--SSQHFYWIGLSYSEEHTAMLWENGSAL
                                                                                                                                                                                                                                                                                                                                                    CSCLVAITLGLLTAVLLSVLLYQWILCOGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                                                                                                                                                                                                                                                                                                                                                         CLSLMA-TLGILLKNSFTKLSVEPAYTPGPNIELQKDSDCCSCHEKWVGYRCNCYFISSE
                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIŠSUE=Blood;
MEDLINE=96011848; PubMed=7589107;
Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
                                                                                                                             (POTENTIAL).

EXTRACTELUIAR (POTENTIAL).

EXTRACTELUIAR (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLONAC. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD94 HUMAN STANDARD;
PRT; 179 AA.
01324I, 04332I, 04373; Q9UBE3; Q9UBEQ0;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
NAV-1997 (Rel. 34, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor)
Netural killer cells antigen CD94 (NK cell receptor)
Netural killer sequence subfamily D, member 1) (KP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB=Placenta;
MEDLINE=98139529; PubMed=9472066;
Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
                                                                                                                                                                                                                                                                                                        19.4%; Score 198.5; DB 1; Length 179; 33.3%; Pred. No. 5.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                                                              69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 --SQYLFPSFETFKPKNCIAYNSKGNALDESCETKNRYICKQ 176
                                                                                                                                                                                                                                                                                     06212B4494527F07 CRC64;
                                                                                                                                                                                                                                                   (in isoform 2).
                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                    L -> LQ (in isofo)
/FTId=VSP_003055.
                                                                                                                                                                                                                              (in isoform 3).
/FTId=VSP_003054.
                                                                                                                                                                                                                                                                                                                   Pred. No. 5.6e; Mismatches
                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
EMBL; AF190933; AAF74529.1; -.
EMBL; AF294886; AAG34498.1; -.
                                                                                                                                                                                                                                                                                     20607 MW;
                                                                                                                                                                                                                                                                                                                              54; Conservative
                                                                                                           10
31
                                                                                                                                                                                                                                                    105
                                                                                                                                                                                                                                                                         139 ]
179 AA;
                      HSSP; P22897; 1EGG
                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    105
                                                                                                                                          32
98
61
89
152
132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLRD1 OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lanier L.L.;
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                                                                                                                                                              DISULFID
                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                              CARBOHYD
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Altansner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubse R.A.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tadokoro K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. Ü.S.A. 99:16899-16903 (2002).
-!- PUNCITION: Plays a role as a receptor for the recognition of MHC class I HALE molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98267245; PubMed=9601951; Futukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tohma S., Inoue T., Yamamoto K., Juji T.; "A alternatively spliced form of the human CD94 gene.";
                                                                                                                                                                                                                                                                                    Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 C-type lectin family domain. DATABASE: NAME=PROW; NOTE=CD guide CD94 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  members.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
Lehrach H., Francis F., Lopez-Botet M.; "Structure of the human CD94 C-Type lectin gene."; Immunogenetics 47:305-309(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing, Named isoforms=3, Name=1; Synonyms=CD94-A; IsoId=Q13241-1; Sequence=Displayed; Name=2; Synonyms=CD94-B; IsoId=Q13241-2; Sequence=VSP_003053; Name=3; Synonyms=CD94 alt, IsoId=Q13241-3; Sequence=VSP 003052; IsoId=Q13241-3; Sequence=VSP 003052; IsoId=Q13241-3; Sequence=VSP 003052;
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Y14288, CAA74663.1, JOINED.
AJ000673, CAA04230.1; -.
AJ000001; CAA03845.1; -.
                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1);
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            MIM; 602894; -.

MIM; 602894; -.

GO; GO:0004888; P:transmembrane receptor activity; TAS.

GO; GO:0004888; P:transmembrane receptor activity; TAS.

GO; GO:0004888; P:transmembrane receptor activity; TAS.

GO; GO:0005860; P:actin aurface receptor linked signal transdu. .; TAS.

InterPro; IPR001304; Lectin C.

Pfam; PR00059; Lectin C.

PRART; SR00034; C. TYPE LECTIN 1; FALSE NEG.

PROSITE; PS00641; C. TYPE LECTIN 2; 1.

PROSITE; PS0041; C. TYPE LECTIN 2; 1.

Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
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                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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LoCOT-2003 (Rel. 42, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
lectin-like receptor subfamily D, member 1).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.2%; Score 196.5; DB 1; Length 179; 32.7%; Pred. No. 8.6e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 --SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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MEDLINE=21623889; PubMed=11751968;
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Genew; HGNC:6378; KLRD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR,01304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                           J. Immunol. 168:240-252(2002).
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytocoxic T-cells.
-!- SUBDNIT: Can form disulfide-bonded heterodimer with NKG2 family
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P.; "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

C-TYDE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

L -> LO (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2; Synonyms=CD94-B;
IsoId=Q9MZ41-2; Sequence=VSP 003056;
-!- TISSUE SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains I C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 --SQYLFPSFETFNPKNCIAYNPNGNALDESCEDKNRYICKQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7244D99E8D9587E7 CRC64;
                                                                                                                                                                                                                         members.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.0%; Score 194.5; DB 1
32.7%; Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  003056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9MZ41-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L -> LQ (i
/FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF259054; AAF86964.1; -. HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AA; 20493 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               092478; Q9BS74; Q9UQB4;
28-FBB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms=CD94-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Conservative
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                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS
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174
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31
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CLE2_HUMAN
ID _CLE2_HU
AC _Q92478;
DT _28-FEB-
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R.A.W.;

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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Torahiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Torahiyuki S., Carninci P., Frange C.,
RA Bas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rahelton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005530; F:lectin; TAS. GO:0006960; P:antimicrobial humoral response (sensu Inver. . ; TAS.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99173880; PubMed=10072769;
Yokoyama-Robayashi M., Yamaguchi T., Sekine S., Kato S.;
"Selection of cDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.";
Gene 228:161-167(1999).
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-type lectin superfamily member 2 (Activation-induced C-type lectin)
CLECSF2 OR AICL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
-!- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues, and in most hematopoietic cell types.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(VGI_TaxID=9606;
                                                                                                                                                                                                                                   MEDLINE=97190245; PubMed=9038101;
Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.
"AICL, a new activation induced antigen encoded by the human NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS0061; C TYPE LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Transmembrane; Lectin; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 603242; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Urinary bladder;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                     Immunogenetics 45:295-300(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB015628; BAA76495.1; -. EMBL; BC005254; AAH05254.1; -. Genew; HGNC:2053; CLECSF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X96719; CAA65480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 CPYDWIGFQNKCYYFSKEEGDWNSSKYNCSTQHADLTIIDNIEEMNFLRRYKCSSDHWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FP-9 / Isolate HP-438;
MEDINTB=88229622; PubMed=2836648;
Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 L---RNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKMAKNRTG-QWVDGA--TFTKSFGMRGSEGCAYLSDDGAATARCYTERKWICRK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20193820; PubMed=10729156;
Achonso C.L., Tulhaman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpow virus.";
J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                        6 ;
                                                                                                                                                                                                                                                        . .) (POTENTIAL)
                                                                                                                                                                                                          (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                     Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of fowlpox virus.";
J. Gen. Virol. 69:1025-1040(1988).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                  0B4FED23424F6C55 CRC64;
                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                          C-TYPE LECTIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLONAC. . .) (1)

N-LINKED (GLONAC. . .) (1)

M -> T (IN REF. 1).

D -> H (IN REF. 1).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P14371; Q9J500; Created) Created) Corresponding Rel. 13, Created) Corresponding Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Putative C-type lectin protein FPV239 (BamHI-ORPS).
                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P05140; ZAFP.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TXPE_LECTIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 8e-10
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 AA
                                                                                                                                                                                                                                                                                                                                                                                     Score 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF198100; AAF44583.1; -.
                                                                                                                                                                                                                                                                                                                                     17307 MW;
                                                                                                                                                                                                                                                                                                                                                                                     17.18;
                                                                                                                                                                                                                                                                                                                                                                                                             32.2%;
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PIR; H29963; WMVZF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-116 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 32.2 37; Conservative
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                                                                        144
144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fowlpox virus (FPV)
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                                                                     26
442
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123
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DOMAIN
TRANSMEM
                                                                                                DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                        CARBOHYD
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                DISULFID
                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                          DOMAIN
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                                                                                                                                                                                                                                                          75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFCWIG 134
                                                                                                                                                                                                                                                                                            48 CKEGWVGYNKNCYFFSEEKNNKSLAVERCKDMDGHLTSISSKEEFKFILRYKGPGNHWIG 107
                                                                                                                                                                                                                                                                                                                                                                              135 LRN---NSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKVRL 189
                                                                                                                                                                                                                                                                                                                                                                                                             108 IEKVDFNGTWKLEDGS--SYDNIVPIKGIGDCAYLSDRSIMSSFCFLPKKWICRIILL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Afonso C.L., Tulman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; "The genome of fowlpox virus."; J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                   s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative C-type lectin protein FPV008/FPV253 (BamHI-ORF2).
FPV008 AND FPV253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Virol. 74:3815-3831(zvvv).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                               18635 MW; 5156DC8928855532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C769ECAA8AD238ED CRC64;
                                                                                                                                   DB 1;
                                                                                                                                         Score 156.5; DB 1
Pred. No. 5.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001304; Lectin_C.
Pfam; PR00059; Lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 AA
                                                                                                                                                                                                   26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TYPE LECTIN.
                                                   C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (St
or send an email to license@isb-sib.ch).
PROSITE; PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20193820; Pubmed=10729156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=FP-9 / Isolate HP-438;
MEDLINE=88229622; PubMed=2836548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fowlpox virus.";
Gen. Virol. 69:1025-1040(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, D00295; BAA00192.1; -.
EMBL, AR198100; AAR44607.1; -.
EMBL, AR198100; AAR44608.1; -.
PIR, B29963; WMVZF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 AA; 19869 MW;
                        Hypothetical protein; Lectin.
DOMAIN 48 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.0%;
25.8%;
                                                                                                                                         15.3%;
26.3%;
                                                                                                                                                                                                      31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                               163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fowlpox virus (FPV)
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avipoxvírus.
NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V008 FOWPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The gent.
T. Virol.
                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P14370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
V008_FOWPV
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIDDER REAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
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                                                              96 WNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRIS 155
Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       absent by
                                                                                     Rafaeloff R., Pittenger G.L., Barlow S.W., Qin X.F., Yan B., Rosenberg L., Duguld W.P., Vinik A.I.; "Cloning and sequencing of the pancreatic islet neogenesis associated protein (INGAP) gene and its expression in islet neogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Clin. Invest. 99:2100-2109(1997).
-!- FUNCTION: Constituent of ilotropin, which is a partially purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1. SUBCELLULAR LOCATION: Secreted (By similarity).
-1. TISSUE SPECIFICITY: EXPRESSED ONLY IN CW ANIMALS PANCREAS AND TO LESSER EXTENT IN DUODENUM. IN PANCREAS IT IS FOUND IN ACINAR CELLS, BUT NOT IN ISLETS.
-1. INDUCTION: Found 1 and 2 days after cellophane wrapping, absent by the 6th day. This period coincides with islet neogenesis.
-1. SIMILARITY: Contains 1 C-type lectin family domain.
-1. CAUTION: It is uncertain whether Met-1, Met-2 or Met-5 is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CW) pancreata. Capable of
a prerequisite for islet
                                                                                                                                                                                                                                                                                                                                                                                             Pancreatic beta cell growth factor precursor (Islet neogenesis associated protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P05451; 1QDD.

G0; G0: 0005576; C: extracellular; NAS.

G0; G0: 0008083; F: growth factor activity; NAS.

G0; G0: 00108083; F: eell growth; NAS.

G0; G0: 00108283; P: cell proliferation; TAS.

InterPro; IPR001394; Lectin C.

InterPro; IPR001399; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                          092778; P70109; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SYNTHESIS OF 104-118
STRAIN=Lake View Golden; TISSUE=Pancreas;
MEDLINE=97296198; PubMed=9151782;
                                                                                                                                             156 SNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                       124 EQGVNDICLLFDTSNIIEMSCIFHERTICVK 154
                                                                                                                                                                                                                                                                                             175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preparation of cellophane wrapping initiating duct cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U41737; AAB86497.1; ALT_INIT.
EMBL; U41738; AAB16754.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00059; lectin c;
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00034; CLECT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hamsters.";
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29; Mismatches

Conservative

39;

Matches

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TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CROHO
                                                                                                                                                                                                DISULFID
                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CROHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHBB
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHBB_(
      SET TETETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                            d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-EROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                        97 -NSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA----FCWIGLR-----NNSGWR 142
                                                                                                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                  2 MLPMTLCRMSWMLLSCLMFLSWVEGEESQKKLPSSRITCPQGSVAYGSYCYSLILIPQTW
                                                                                                                                                                                                                                                                            38 LVAITLGLLTAVLLSVLLY-QWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDW
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intestine, moderately in colon and at an extremely low level in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure, chromosomal localization and expression of mouse genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: Might be a stress protein involved in the control of bacterial proliferation.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Constitutively expressed in the small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
Gene 185:159-168(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                   143 WEDGSPLNFSRISSNSFVQT----CGAIN-KNGLQA---SSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | : | | : | | : | | 172 | | 172 | | | 172 | | | 172 | | | 172 | | | 172 | | 172 | | 172 | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | | 173 | 
                                                             GROWTH FACTOR.
                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/61; TISSUB=Liver, and Pancreas; MEDLINE=97208868; PubMed=9055810; Marushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H., Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
                                                                                                                                                                                                  Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pancreatitis-associated protein 3 precursor (REG III-gamma) PAP3 OR REG3G.
                                                                                                                                                                                                                                       Indels
                                                       PANCREATIC BETA CELL GROWTH
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        healthy pancreas. SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                         3854F36BA35D17CE CRC64;
                                                                                                                                                                                                                                     72;
                                                                                                                                                                                                Score 147.5; DB 1;
Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA
                                                                                                                                                                                                                                       Mismatches
                                        BY SIMILARITY
PROSITE; PS50041; C_IYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:109406; Reg3g.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
                                                                                                                                                           19940 MW;
                                                                                                                                                                                                14.4%;
24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D63362; BAA18931.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D63361; BAA18930.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003990; Pancres
Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                       42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                      26
175
173
51
171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                         175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P05451; 1LIT
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                         27
38
40
68
146
                    Signal; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAP3 MOUSE
009049;
                                                                                                                DISULFID
DISULFID
SEQUENCE
                                                                                                DISULFID
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                     Local
                                        SIGNAL
                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAP3_MOUSE
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---
  STTTTTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 YDADMACQKRPSGHLVSVLSGAEASFLSSMIKSSGNSGQYVWIGLHDPTLGYEPNRGGWE 121
                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
     PRINTS; EMOUSA; CECT; 1.

SMART; SMOODSA; CLECT; 1.

PROSITE; PSOOGLS; C TYPE LECTIN 1; FALSE_NEG.

PROSITE; PSOOGLS; C TYPE_LECTIN_2; 1.

Signal; Lectin; Inflammatory response; Acute phase; Multigene family.

SIGNAL 1 26 POTENTIAL.

CHAIN 27 174 PANCREATITIS-ASSOCIATED PROTEIN 3.

CHAIN 27 174 C-TYPE LECTIN (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding, and stimulates agglutination.
--- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
--- SUBCELLULAR LOCATION: Secreted.
--- SINLARITY: Contains I C-type lectin family domain.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LPRITITIMSWMLLSCLMLLSQVQGEVAKKDAPSSRSSCPKGSRAYGSYCYALFSVSKWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 NSSLEFCLARDS-HLLVITDNQEMSLLQVFL----SEAFCWIGLR------NNSGWR
                                                                                                                                                                                                                                                                                                                                                                                                                         38 LVAITLGLLTAVLLS-VLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M., Smith A.I., Lopez J.A., Berndt M.C.;
Smith A.I., Lopez J.A., Berndt M.C.;
Binding of a novel 50-kilodalton alboagregin from Trimeresurus
albolabris and related viper venom proteins to the platelet membrane
glycoprotein ID-IX-V complex. Effect on platelet aggregation and
glycoprotein ID-mediated platelet activation.";
Biochemistry 35:12629-12639(1996).
-!- FUNCTION: Binds to platelet GPiB/IX receptor system, inhibits VWF
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crotalus horridus horridus (Timber rattlesnake).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 WEDGSPLNFSRISSN---SFVQTCGAINK-NGL---QASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 WSNADVMNYINWETNPSSSGNHCGTLSRASGFLKWRENYCNLELPYVCK 171
                                                                                                                                                                                                                                                                                                                            Length 174;
                                                                                                                                                                                                                                                                                                                       ; Score 147; DB 1; Length 174; Pred. No. 4.5e-07; 30; Mismatches 73; Indels
                                                                                                                                                                                                                                                                      5575E9E56A4D8CEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CHH-B beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA
                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-TYPE LECTIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                       14.4%; Score 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96420502; PubMed=8823201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00059; lectin_c; 1._
PRINTS; PR00356; ANTIFREEZEII.
PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                           19307 MW;
                                                                                                                                                                                                                                                                                                                                                 26.5%;
                                                                                                                                                                                                                                                                                                                                                                        45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                           26
174
172
51
170
162
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13
115
92
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                                                                                                                                             27
38
40
40
68
145
174 AA;
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9229
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InterPro; IPR003990; Pancreatis ac.
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Les 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REG1 OR REG.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LITH RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P10758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LITH_RAT
      DAR AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AND RANGE AN
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                                                                                                                                   ب<u>.</u>
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                                                                                                                                                                                    75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDS--HLLVITDNQEMSLLQVFLSEAFCW 132
                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                        133 IGLR---NNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANCREATIC ACINAR CELLS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: Constitutively expressed in the small intestine, moderately in colon and at an extremely low level in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TSSORE-Bancreas, and Small intestine;
MEDLINE=93176807; Pubmed=7679928;
Itch T., Teraoka H.;
Cloning and tissue-specific expression of cDNAs for the human and mouse homologues of rat pancreatitis-associated protein (PAP).";
Biochim. Biophys. Acta 1172:184-186(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                healthy pancreas.
-!-INDUCTION: Appears in pancreatic juice after induction of pancreatic inflammation.
-!-INDUCTION: Appears of pancreatic inflammation.
-!- DISEASE: Overexpressed during the acute phase of pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure, chromosomal localization and expression of mouse genesencoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma."; Gene 185:159-168(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Might be a stress protein involved in the control bacterial proliferation.
                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=97208868; PubMed=9055810;
Narushima Y., Umno M., Nakagawara K.-I., Mori M., Miyashita H.,
Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yozekura H.,
                                                           14.3%; Score 146; DB 1; Length 117; 28.4%; Pred. No. 3.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 1 precursor (REG III-beta).
                                                                                                                            57; Indels
13888 MW; 07835BBCB61E9EAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 AA
                                                                                                                         20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S29822; S29822.
HSSP, 905451; ILIT.
HSSP, MGI:97478; Pap.
INTERPRO; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D13509; BAA02727.1; -. EMBL; D63359; BAA18928.1; -. EMBL; D63360; BAA18929.1; -.
                                                                                                                         33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAP OR PAP1 OR REG3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
117 AA;
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAP1 MOUSE
P35230;
SEQUENCE
                                                       Query Match
                                                                                                                         Matches
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89 FSVEEKDWNSSLEFCLAR-DSHLLVITDNQEMSLLQVFL----SEAFCWIGLR----- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 --NNSGWRWEDGSPLNFSRISSNSFVQT----CGAINK-NGL---QASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 EPNGGGWEWSNNDVMNYFNWERNPSTALDRAFGGSLSRASGFLKWRDMTCEVKLDYVCK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PRODOGIS; CTYPE LECTIN 1; 1.

PROSITE; PSSO041; CTYPE LECTIN 2; 1.

PROSITE; PSSO041; CTYPE LECTIN 2; 1.

SIGNAL 1 26 BY SIMILARITY.

CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 1.

DOWALN 38 173 C-TYPE LECTIN (LONG FORM).

DISULFID 40 51 BY SIMILARITY.

DISULFID 68 171 BY SIMILARITY.

DISULFID 146 163 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SCPDRWMKYGNHCYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FBB-2003 (Rel. 41, Last annotation update)
hithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic
thread protein) (PTP) (Islet of langerhans regenerating protein) (REG)
(Islet cells regeneration factor) (ICRF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91093273; PubMed=1985964;
Rouquier S., Verdier J.M., Iovanna J., Dagorn J.-C., Giorgi D.;
"Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocrine cells, regulation by food content, and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 175;
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Miyashita H., Suzuki Y., Watanabe T., Unno M., Moriizumi S.,
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"A novel gene activated in regenerating islets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                              44B3101171E79775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 PSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYSTCASCP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 137.5; DB 1;
25.7%; Pred. No. 3.7e-06;
ive 28; Mismatches 70;
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J. Biol. Chem. 266:786-791(1991).
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01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
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Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
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DOMAIN
DISULFID
DISULFID
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license gareement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                         MEDILINE 90031455; PubMed=2680252;
Adrich Z., de Caro A.M., Guidoni A.A., Woudstra M.E., Rovery M.;
"Characterization in rat pancreatic juice of a protein homologous to
the human pancreatic stone protein.";
Comp. Biochem. Physiol. 93B:793-797(1989).
-!- FUNCTION: Might act as an inhibitor of spontaneous calcium
carbonate precipitation.
-!- TISSUE SPECIFICITY: Expressed only in regenerating islets, but
not in normal pancreatic islets, insulinomas or regenerating
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C-TYPE LECTIVE BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
W, 9B61EB236B82CF8A CRC64;
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                     gene.";
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Last annotation update)
               "Structure and characterization of rat Reg I Seikagaku 65:1082-1082(1993).
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PRINTS, PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Glycoprotein; Signal; Lectin.
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InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
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27.2%; Pre
tive 23;
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EMBL; M62930; AAA41974.1; -.
EMBL; M18962; AAA42028.1; -.
EMBL; D26164; BAA05149.1; -.
PIR; A28351; A28351.
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Okamoto H.;
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35
63
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129
165 AA;
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Matches 43; Congery
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P05140;
13-AUG-1987
01-AUG-1990
28-FEB-2003
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ANP HEMAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFIDE BONDS, AND SIMILARITY TO C-TYPE LECTINS.
MEDLINE=92355557; PubMed=1644794;
NG N.F.L., Hew C.-L.;
"Structure of an antifreeze polypeptide from the sea raven. Disulfide bonds and similarity to lectin-binding proteins.";
J. Biol. Chem. 267:16069-16075(1992).
                                                                                                                                                                                                                                                                                                                                MEDLINE-87057207; PubMed=3782083;
Ng N.F.L., Trinh K.-Y., Hew C.-L.;
"Structure of an antifreeze polypeptide precursor from the sea raven,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90036986; PubMed=2572595;
Hayes P., Scott G.K., Ng N.F.L., Hew C.-L., Davies P.L.;
Hayes P., Scott G.K., Ng N.F.L., Hew C.-L., Davies F.L.;
Hoyatine-rich type II antifreeze protein precursor is initiated from the third AUG codon of its mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98206886; PubMed=9537986; Groundly W., Loewen M.C., Lix B., Daugulis A.J., Soemichsen F.D., Groundl W., Loewen M.C., Lix B., Daugulis A.J., Soemichsen F.D., Davies P.L., Sykes B.D.; "The solution structure of type II antifreeze protein reveals a new member of the lectin family."; Biochemistry 37:471(1998).

-i. FUNCTION: Antifreeze proteins lower the blood freezing point.
-i. SIMILARITY: BELONGS TO THE TYPE-II AFP FAMILY. TYPE 2 AFP ARE
Antifreeze protein precursor (AFP).

Hemitripterus americanus (Sea raven).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;

Cottoidei; Hemitripteridae; Hemitripterus.
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PROSITE; PS50041; C TYPE LECTIN 2; 1.
Antifreeze protein; Lectin; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 261:15690-15695(1986).
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PIR; AA4313; A34313.
PDB; 2APP; 23-DEC-98.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
Pfan; PP00059; lectin_C; I.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; I.
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                                                                                                                                                                                                                                                                                                                                                                                39 PNCPAGWQPLGDRCIYYETTAMTWALAETNCMKLGGHLASİHSQEEHSFIQT-LNAGVVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thread protein) (PTP) (Islet of langerhans regenerating protein) (REG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90368981; PubMed=2394826; de la Monte S.M., Ozturk M., Wands J.R.; de la Monte S.M., Ozturk M., Wands J.R.; "Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease and the developing human brain."; J. Clin. Invest. 86:1004-1013(1990).
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-ROV-1991 (Rel. 41, Last sequence update)
Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross J., Brauer A.W., Bringhurst R.F., Corbett C., Margolies M.N., "An umusual bowine pancreatic protein exhibiting pH-dependent globule-fibril transformation and unique amino acid sequence.", Proc. Natl. Acad. Sci. U.S.A. 82:5627-5631(1985).
-!- FUNCTION: Might act as an inhibitor of spontaneous calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Cleaved to give an A chain and a B chain joined by
                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cai L., Harris W.R., Marshak D.R., Gross J., Crabb J.W.; "Structural analysis of bovine pancreatic thread protein."; J. Protein Chem. 9:623-632(1990).
                                                                                                                                                                                                                                                             Length 163;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                       52C2D284F65E8A47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disulfide bond.
-!- TISSUE SPECIFICITY: In pancreatic acinar cells.
                                                                                                                                                                                                                                                             th 13.3%; Score 136; DB 1; Similarity 31.7%; Pred. No. 4.7e-06; 26; Conservative 10; Mismatches 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells regeneration factor) (ICRF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 İGGSACLQAGAWTWSDGTPMNF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           133 IG---LRNNSGWRWEDGSPLNF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91197388; PubMed=2085387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 38-85 AND 141-175.
MEDLINE=85298214; PubMed=3862086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 38-138 AND 141-175
                                                                                                                                                                                                                       17509 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
76
91
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1146
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                                                                                                                                                                                                                       163 AA;
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 TLGL--LTAVLLSVLLYQWILCQGSNYSTCASCP----SCPDRWMKYGNHCYYFSVEEKD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 WMDADIACQKRPSGHLVSVLSGAEESFVASLVRNNLNTQSDIWIGLHDPTEGSEANAGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 WNSSLEFCLARDS-HILVITDNQEMSLLQVFL----SEAFCWIGLR------NNSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 2 precursor (Lithostathine 3) (Islet of langerhans regenerating protein 3) (REG 3) (REG III-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 RWEDGSPLNF----SRISSNSFVQTCGAINKNG----LQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 EWISNDVLNYVAWETDPAAISSPGY---CGSLSRSGGYLKWRDHNCNLNLPPYVCK 172
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    -!- SUBCELLULAR LOCATION: Secreted.
    -!- TISSUE SPECIFICITY: Small intestine and pancreas.
    -!- DISEASE: Overexpressed during the acute phase of pancreatitis.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamoto H.;
"Structure, chromosomal localization and expression of mouse genes encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
Gene 185:159-168(1997)
-!- FUNCTION: Might be a stress protein involved in the control of bacterial proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/61; TISSUE=Liver, and Pancreas;
MEDLINE=97208868; PubMed=9055810;
Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
  Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                 A CHAIN.
B CHAIN.
C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C270EE70B7E91D6A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 134.5; DB 1
Pred. No. 7.1e-06;
modified and this statement is not removed.
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BY SIMILARITY.
EE -> FF (IN R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Mismatches
                      entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                      HSSP, P05451; 10DD.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Panoreatis_ac.
Pfam, PR00059; lectin_c; 1.
PRINTS; PR01504; PWCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                             EMBL; M59794; AAA30750.1; -.
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                                                                                                                    PIR; A37194; A37194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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DISULFID
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SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 SLEFCLARDS-HILVITDNQEMSILQVFLSEAF----CWIGLR-----NNSGWRWE 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.;
Suzuki M., Matsui T., Titani K., Yoshioka A.;
"The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromboffii venom.";
Thromb. Haemost. 79:1199-1207(1998).

Thromb. Haemost. 79:1199-1207(1998).

-I- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ITLGLLTAVLLSVLLYQWILCQGSNYSTCASCP--SCPDRWMKYGNHCYYFSVEEKDWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                            Signal, Lectin, Inflammatory response, Acute phase, Multigene family. SIGNAL

1 26 BY SIMILARITY.
CHAIN 27 175 PANCREATITIS-ASSOCIATED PROFEIN 2.
DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
DISCULPID 40 51 BY SIMILARITY.
DISCULPID 68 171 BY SIMILARITY.
DISCULPID 146 163 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 DGSPLNF----SRISSNSFVQTCGAINKNGLQASS------CEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%; Score 134.5; DB 1; Length 175; 28.2%; Pred. No. 7.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Mamushigin beta chain precursor.
Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69; Indels
 SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3E311B3976E80F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Mismatches
                                                                                                                                                                                                                                                                  Pfam; PF00059; lectin c; 1.
PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                    MGD; MGI:109408; Reg3a.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            19539 MW;
                                                                                                                                                         EMBL; D63356; BAA18925.1; -. ERNBL; D63357; BAA18926.1; -. EMBL; D63358; BAA18927.1; -. HSSP; P05451; 1LIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCL--ARDSHLLVITDNQE----MSLLQVFLSE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AFCWIGLRNNSGW-----RWEDGSPLNFSRISSNSFVQTCGAI-----NKNGLQASSCEVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 DEVWIGL--NNIWNECMVEWIDG----TRLSHNAWITESECIAAKTIDNQWLSRPCSRT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 CPSDWSSYEGHCYRVFQKEMTWEDAEKFCTQQRKESHLVSFHSSEEVDFVVSMTWPILKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH C-103 IN ALPHA CHAIN) (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted.
MASS SPECTROMETRY: MW=15413; MW_ERR=6; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 134; DB 1; Length 14
28.6%; Pred. No. 6.5e-06;
ive 18; Mismatches 50; Indels
                                                                                SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9EDA84BDCC24E76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAMUSHIGIN BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                        HSSP; P23807; IIXX.
GO; GO:0005576; C:extracellular; IC.
GO; GO:0005786; P:blood coagulation; IDA.
GO; GO:0007304; Lectin_C.
Pfam; PF00059; lectin_c; l.
SMARY; SM0034; CLECT; l.
PROSITE; PS00615; C_TYPE_LECTIN_1; l.
PROSITE; PS50041; C_TYPE_LECTIN_2; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
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143
36
142
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                                                             RANGE=24-146.
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DISULFID
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August 10, 2004, 16:29:18; Search time 37 Seconds (without alignments) 1611.701 Million cell updates/sec
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1 MTDSVIXSMLELFTATQAQN......GLQASSCEVPLHGVCKKVRL 189
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 1017041 seqs, 315518202 residues
                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
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sp_human:*
             Copyright
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Maximum DB seq length: 189
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	O43198 homo sapien	075613 homo sapien	088713 mis misculi	064335 rattus norv	Ognzsl homo sapien	091zwg musculu	O8mii3 opnog Sirma	O8mhv8 opnog opnog	035778 ratting norv	O8mbva opnog evdm80	O8mii4 condo Airma	O8r4k5 rattus norv	O9dk90 macaca mila	Ospan Sils scrofa	080287 0811118 0811	O54708 mus musculu
SUMMARIES			OT .	043198	075613	088713	064335	O9NZS1	091ZW9	QBMJI3	OBMHY8	035778	QBMHY9	QBMJ14	Q8R4K5	Q9GK90	OBSPXO	080287	054708
			DB	4	4	11	11	4	11	9	9	11	9	9	11	9	9	13	11
			Match Length DB	189	189	188	188	181	178	179	179	179	179	179	132	163	159	183	179
	•₩•	Query	Match	100.0	98.4	53.6	51.4	22.0	19.0	18.5	18.5	18.3	18.2	18.2	18.1	18.1	18.0	18.0	17.9
			Score	1023	1001	548.5	525.5	225	194.5	189.5	189.5	187	186.5	186.5	185	185	184.5	184	183.5
		Result	No.	Н	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16

054707 mus musculu Q80z35 mus musculu Q9jkf2 mus musculu Q95j54 pan troglod	95)94 bos caurus Q95)4f3 mus musculu Q9mzj6 macaca mula Q95j96 bos taurus Q95j95 bos taurus	Q9ep94 mus musculu Q7tsp6 mus musculu Q8mjh4 pongo pygma Q8mjh3 pongo pygma Q9hd37 homo sapien	Q8mhy4 pongo pygma Q7t045 vipera lebe Q9glf4 sus scrofa Q9ny25 homo sapien Q8ize9 homo sapien Q8wup7 homo sapien	Q8vil9 mus musculu Q8bhf7 mus musculu Q9ukq0 homo sapien Q61972 mus musculu Q9G1f8 sus scrofa Q96pa7 homo sapien Q9xx3 hydra magni Q9d8q7 mus musculu
11 054707 11 080235 11 09UKF2 6 095U54		11 QYEF94 11 QYTSP6 6 Q8MJH4 6 Q8MJH3 4 Q9HD37	୍ଷ ପର୍ବର ଆ	11 Q88V119 12 Q8BHK7 13 Q61972 14 Q8CJ86 15 Q9GLF3 17 Q96PA7 17 Q9D8Q7
	175 1 175 1 185 6 80 6		, ,	142 1 142 1 142 1 142 1 168 1 134 4 1 76 1
17.9 17.6 17.2	16.9 16.9 1.6.0	15.8 15.8 15.8	1125.66.7 125.56.66.7	1155.2 115.2 115.2 114.3 114.3 114.3
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ALIGNMENTS

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TISSUE-Lung;

XMEDLINE-9848735; PubMed=9765598;

Amenia MAFA has alternatively spliced variants.";

Lamena MAFA has alternatively spliced variants.";

Biochim. Biophys. Acta 1399:209-212(1998).

Biochim. Biophys. Acta 1399:209-212(1998).

Robis Afortological to membrane; TAS.

GO; GO:0003793; F:defense/immunity protein activity; TAS.

RO; GO:0004872; F:receptor activity; TAS.

RO; GO:0004872; F:receptor activity; TAS.

RO; GO:0005868; P:cell surface receptor linked signal transdu. .; TAS.

RO; GO:0006954; P:inflammatory response; TAS.

RO; GO:0006959; P:cell are defense response; TAS.

RO; GO:0006959; P:cell cell are defense response; TAS.

RO; GO:0006959; P:cell cell are defense response; TAS.
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                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 1023; DB 4; Length
Best Local Similarity 100.0%; Pred. No. 7.4e-105;
Matches 189; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
149 AA; 21079 MW; TSE042AD40B2B4F6 CRC64;
                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mast cell function-associated antigen.
                                      189 AA.
                                    PRT;
                                    PRELIMINARY;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID=9606;
                              043198
RESULT 1
                   043198
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1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60

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PRELIMINARY;
                                                             like receptor G1).
KLRG1 OR MAFA.
                                                                                                          NCBI_TaxID=10090;
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                 088713;
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                          120
                                                                               LLOVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                               LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
MIDSVIYSMLELPIATQAQNDYGPQQKSSSSKPSCSCLVAITLGILTAVLLSVLLSVQIL
                           COGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS
                                      CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                  Butcher S., Arney K.L., Cook G.P.; "MARA-L, an ITM-containing receptor encoded by the human NK cell complex and expressed by basophils and NK cells."; Eur. J. Immunol. 28:0-0(1998).
                                                                                                                                                                                                                                      nomo saplema (manun).
Eukaryota; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.4%; Score 1007; DB 4; Length 189; 98.4%; Pred. No. 4.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            PSS0041; C_TYPE LECTIN 2; 1.
189 AA; 21206 MW; FA9023F1523656A8 CRC64;
                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                               ITIM-containing receptor MAFA-L.
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Matches 186; Conservative
                                                                                                                                                                  PRELIMINARY;
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                                                                                                    HGVCKKVRL 189
                                                                                                                     HGVCKKVRL 189
                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRALM-C.B-17 SCID;
MEDILINE=99077114; PubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
Hanke T., Corral L., Vance R.E., Faulet D.H.;
Ist antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRANIE-129/SevTACEBL; TISSUB-Spleen;
MEDLINE=115136; PubMed=11220622;
Voehringer D., Kaufmann M., Pircher H.;
VGenomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor Gl gene (KLRG1), the mouse homologue of MARA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSL-RILTNSLIQRCGAIHRNGLQASSCEVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-AUG-12003 (TrEMBLrel. 25, Last amnotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lectin; Receptor. - - - 876336802EA134F1 CRC64; SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ0107357, AAD03718.1, ...
EMBL; AJ010751, CAA09342.1; ...
EMBL; AJ010727, AAX40082.1; ...
MCD; MC1:1355294; Klrg1.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007127; F:sugar binding; IEA.
InterPro; IPR001304; Lectin. C.
InterPro; IPR001304; Lectin. C.
EMBL; AG0003055; Lectin. C.
EMBL; AD0003055; Lectin. C.
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55.6%; Pred. No. 2.1e-52;
tive 26; Mismatches 56;
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188 AA
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PRT;
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Matches 104; Conservative
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                                                                                                                                                                                                                                     Mus musculus (Mouse).
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Q64335;
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ID Q6
AC Q6
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"Human KLRRI, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis."; Eur. J. Immunol. 30:568-76(2000).
                                                                                                                              GO; GO:0016020; C:membrane; TAS.
GO; GO:0030106; F:MHC class I receptor activity; TAS.
InterPro; IPRO01304; Lectin_C.
EMBRH; PRO0059; lectin_C; 1.
SWART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
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InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
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EMBL, AF373410; AAL13236.1; -.
MGD; MGI:2157945; Cd209c.
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.6%;
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Les 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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    Fernandez-Ruiz E.;
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NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLS-ILSNSVVQKCGTIHRCGLHASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQGSNYSTCASCPSCPDRWMKYGNHCYYPSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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MEDIJNE=96016176; PubMed=7568140;
Guthmann M.D., Tal M., Pecht I.;
Guthmann M.D., Tal M., Pecht I.;
"A secretion inhibitory signal transduction molecule on mast cells is another C-type lectin.";
Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).

EMBL; X97191; CAA65829.1; JOINED.

EMBL; X97193; CAA65829.1; JOINED.
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=20135860; PubMed=10671213;
Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                       STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
Bocek Jr P., Guthmann M.D., Pecht I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART: SM00034; CLCT; 1.
PROSITE; PS50041; CLCT; 1.
SROUNCE 188 AA; 21356 MW; ZCC8032D4D020B15 CRC64;
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  Created)
Last sequence update)
Last annotation update)
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EMBL, X97195; CAA65829.1; JOINED.
EMBL, X79812; CAA56208.1; -
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01-0CT-2000 (TrEMBLrel. 15,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 53.5*
Matches 100; Conservative
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                                                                                                             Rattus norvegicus (Rat)
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=10116;
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                                                                    MAFA protein.
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 GLLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFC
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Matsuda Y., Clausen B.E., Inaba K., Steinman R.M.;
"Five mouse homologues of the human dendritic cell C-type lectin, DC-
                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                            Length 181;
                                                                                                                                                            22.0%; Score 225; DB 4; Length 18
33.6%; Pred. No. 1.1e-16;
tive 26; Mismatches 45; Indels
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PROSITE; PS50041; C TYPE LECTIN 2; 1.
SEQUENCE 178 AA; 21245 MW; 034F94CE02BD9032 CRC64;
181 AA; 21204 MW; 64642240CAE1E551 CRC64;
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Last annotation update)
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82 YGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNN 138
                                       MEDIME=22072192; PubMed=12077248; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; NIX Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Dissen E., Berg S.F., Westgaard I.H., Fossum S.;
"Molecular characterization of a gene in the rat homologous to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 SGWRWEDGSPLN-----FSRISSNSFVQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.5%; Score 189.5; DB 6; Length 179; 28.6%; Pred. No. 9.4e-13; Live 29; Mismatches 61; Indels 35;
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20781 MW; 11E6A55C670EE84C CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                    GO; GO:0004872; F:receptor activity; IEA. GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                 InterPro; IPR006209; EGF_like...
InterPro; IPR001304; Lectin_C.
Pfam, PF00059; lectin_c; 1.
SMARY; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
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EMBL; AF009133; AACL0220_11; -
GO: GO:0005529; F:Sugar binding; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; LecTin_C.
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EMBL; AF470381; AAM78481.1; -.
EMBL; AF470382; AAM78482.1; -.
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01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSS0041; C TYPE LEC
PROSITE; PS00022; EGF_1; 1.
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Best Local Similarity
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                      SEQUENCE FROM N.A.
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                                                                                                                                        with MHC-C.";
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SEQUENCE
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                   CWIG---LRNNSGWRWEDGSPLNFSRIS----SNSFVQTCGAINKNGLQASSCEVPL 180
                                               82 YGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 YRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEH 125
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11 LISGTLGIICLSLMATL---GILLKNSFTKLSIEPAFTPGPDIELQKDSDCCSCQEKWVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22072192; PubMed=12077248; Guethlan L.T., Adams E.J., Parham P.; Meterbion L.A., Flodin L.R., Adams E.J., Parham P.; N.K. Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 LVAITLGLLTAVLLSVLLYQWILCQGS------NYSTCASCPDRWMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat.
Natural killer cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%; Score 189.5; DB 6; 28.6%; Pred. No. 9.4e-13; ive 29; Mismatches 61;
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EMBL; AF470384; AAM78484.1; --
GO, GO:0004872; F:seceptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
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SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
PROSITE; PS00022; EGF 1; 1.
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POPY-CD94.
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                                                                                                               HGVCKK 186
                                                                                                                                                            YWICKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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01-OCT-2002
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SEQUENCE
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Q8MJI3;
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pygmaeus (Orangutan).
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Best Local Similarity
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   YSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVF 125
                                      : : | : | : | : | : | : | : | EXCYPTSKERKSWKGSREFCASQNSSLLQTRNELSFMS-- 109
                                                                                                                              175
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MEDLINE=22072192; PubMed=12077248;
MEDLINE=22072192; PubMed=12077248;
Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pongo.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-07T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell receptor.
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2e-12;
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BENEL, RF470380; AM708480.1; -.
EMEL, RF470385; AAM76485.1; -.
GO, GO:0004872; F:receptor activity; IEA.
GO, GO:005529; F:sugar binding; IEA.
InterPro; IPR005209; BGF like.
InterPro; IPR001304; Lectin_C.
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SMART; SMOR34; CLECT; 1.
PROSITE; PS50041; C TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF 1; 1.
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Q8MHY9
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82 YGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNN 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NYSTCASCPSCPDRWMK
                                                                                                                                     Guethlein L.A., Flodin L.R., Adams B.J., Parham P.; "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TAWLWENGSSLSQYLFPLFETFNP----KNCLAYNPNGNALDESCEDKNRYLCKQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 SGWRWEDGSPLN-----FSRISSNSFVQTCGALNKNG-LQASSCEVPLHGVCKK 186
  Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AA; 15000 MW; 9FFF06A1E23D275C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            674489E5EC6F8780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.2%; Score 186.5; DB 6; 28.6%; Pred. No. 2e-12; iive 28; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 185; DB 11;
Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 LVAITLGLLTAVLLSVLLYQWILCQGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132
                                                                                                                                                                                                                                  J. Immunol. 169:220-229 (2002).

EMBL, AF470383; AAM78483.1; -.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0005529; F:sugar binding; IEA.

InterPro; IPR00529; EGF like.

InterPro; IPR001304; LecLin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00059; lectin c; 1.—
SMARI; SM00034; CLECT; 1.
PROSITE; PS5041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF.1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                                                                              SEQUENCE FROM N.A. MEDLINE=22072192; PubMed=12077248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AA; 20536 MW;
Bukāryotā; Metazoa; Chordata;
Mammalia; Butheria; Primates;
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.1%;
31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 28.6
nes 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD69 (Fragment).
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7;

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74 SCPDRWMKYGNHCYYFSVEEXDWNSSLEFCLARDSHLLVITDNQE-MSLLQVFLSEAFCW 132
                                                                                                                                                                                                                                                                                                                                                                                             43 SCPDDWIGYQTRCYFISKKTKNWTLAQSFCSKHHGATLALLESKEDWVFLKQHVGRAEHW 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 YGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLQVFLSEAFCWIGL---RNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 PQGKCYYLSKEENDWNSSREHCNAHGASLATIGSAEEMDFMMRFQGPANCWIGLHWEEED 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 YGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 HGTGRRRSRVQLIAACAALGTLSLVLVVISTDFAH-----ACPNAWVG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 IGLRNNSG--WRWEDGSPLN--FSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaiser P.;
"Analysis of part of the chicken Rfp-Y region reveals two novel lectin genes, the first complete genomic sequence of a class I alpha-chain gene, a truncated class II beta-chain gene, and alarge CR1 repeat."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, A.277927; CAD61337.1; -..
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0005529; Antifreezell.

InterPro; IPR002353; Antifreezell.
         "Molecular cloning, expression pattern, and chromosomal mapping of pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 SGWRWED-----GSPLNFSRISSNSFVQTCGA----INKNGLQASSCEV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 ALWIWSNVTAFINWRGSP-----SFSQCIGAAFPFSSLLGTGL---SCEV 177
                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,
                                                                                                                                                                                                                                                                      Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.0%; Score 184; DB 13; Length 183; 29.3%; Pred. No. 3.9e-12; Live 20; Mismatches 57; Indels 46
                                                                                                                                                                                                                                                                                                                 Indels
                                                       Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                           EMBL, AF484234; AAL91547.1; -. (
GO, GO.005229; F:sugar binding; IEA.
InterPro; IRR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CIECT; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
SEQUENCE 159 AA; 18056 MW; Ā19C3EBBAE92AA69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 AA; 20011 MW; 725DB7845867D341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                 18.0%; Score 184.5; DB 6; 32.2%; Pred. No. 2.9e-12; ive 19; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-type lectin.
Y-LEC1.
                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  080257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
Q802S7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
            ð
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         3;
                                              SCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 QWILCQGSNYSTCAS----CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 VITDNQEMSLLQVFLSEAFCWIGL-RNNSGWRWEDGSPLNFSRISSNS--FVQTCGAINK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21158386; PubMed=11261935;
Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative
                                                                                                                                     134 GLRNNSG--WRWEDGSPLN--FSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Sus.
       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
    52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
Rothschild M.F., Kim Y.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 163 AA; 18651 MW; DA2C8EA027A4D543 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type II membrane protein CD69 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing of 5' exons in rhesus monkey decidua.";
Immunogenetics 53:69-73(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 185; DB 6; 31.4%; Pred. No. 2.7e-12; ive 24; Mismatches 60
                                                                                                                                                                                                                                                                                                             Ą
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; ĀF294887; AAG34499.1; -.
HSSP; P22897; 1EGG.
GO; GO:0005529; F:sugar binding; 1EA.
                                                                                                                                                                                                                                                                                                                                                      Created)
    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 NGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 RGLKSNQCESTVIYHCK 160
                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 31.4 Matches 43; Conservative
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=9823;
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8SPX0
Q8SPX0;
                                                                                                                                                                                                                                                                                                                                09GK90;
                                                                                                                                                                                                                                                                                                        09GK90
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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Search completed: August 10, 2004, 16:34:58 Job time : 43 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
              Copyright
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using sw model OM protein - protein search,

August 10, 2004, 16:19:43; Search time 53 Seconds (without alignments) 1007.575 Million cell updates/sec Run on:

US-09-811-367B-1

1023 1 MTDSVIYSMLELPTATQAQN.....GLQASSCEVPLHGVCKKVRL 189 Title: Perfect score: Sequence:

Scoring table:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1084940

Minimum DB seq length: 0 Maximum DB seq length: 189

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1980s:* geneseqn1990s:* geneseqn2001s:* geneseqn2001s:* geneseqn2002s:* geneseqn2003s:* geneseqn2003bs:* A Geneseq 29Jan04:* 4.0.0 2.0 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	scri	Aaw88265 Human mas	9 Human ma	Binding	0	Mammalia			Aaw88267 Human MAF	Aar77472 Partial s	Human MA	Aam14192 Peptide #			Abb27967 Human pep	Abb18604 Protein #	Aam66323 Human bon	Aam53935 Human bra	Abq47989 Human liv	Peptid		Human	Abp47880 Human pol	Human	1 Human	2 CD94.
SUMMAKIES	di	AAW88265	AAE11759	ADD25635	AAE11760	AAR77033	AAW88277	AAE11761	AAW88267	AAR77472	AAW88266	AAM14192	ABB33139	AAM26602	ABB27967	ABB18604	AAM66323	AAM53935	ABG47989	AAM01928	ABG35971	AAU19660	ABP47880	ADC10842	AAW64791	AAW40222
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	Length	189	189	189	188	188	188	188	66	114	70	32	35	35	35	35	32	35	35	32		8	8	8	179	7
₩	Query Match	100.0	100.0	98.4	53.6	51.4	51.4	51.4	42.1	36.2	30.0	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	19.2	19.2
	Score		1023	1007			525.5	525.5	431	370.5	306.5	217	217	217	217	217	217	217	217	217	27				196.5	196.5
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Ade76965 Human pro Aam80296 Human pro Abg72616 Human cyt Aam80302 Human pro	Aaw63020 Mouse dec Aaw5857 Protein e Aaw64544 Human lym Aaw75877 Iype II m	Aaw85592 Human C-t Abb09713 Amino aci Adc38674 Human sec Aaw63018 Mouse dec	Mouse Human Human Human	Aau72821 Human NKG Aau72820 Human NKG Aau19836 Human nov Aau19690 Human nov
ADE76965 AAM80296 ABG72616 AAM80302	AAW63020 AAW36957 AAW64544 AAW75877	AAW85592 ABB09713 ADC38674 AAW63018	AAW63019 AAU79037 ADD18706 AAU72822	AAU72821 AAU72820 AAU19836 AAU19690
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196.5 180 180 180	175.5 175 175 175	175 175 175 173	172 168 168 166	166 166 165 165
222 238 298	30 33 33	3.4 3.5 3.5 7.5	38 39 40 11	4 4 4 4 2 6 4 3

ALIGNMENTS

RESULT 1

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Mast cell function-associated antigen, MAFA, splice variant, human, inflammation, allergy, asthma; rheumatoid arthritis, tumour, therapy.
                                                  Human mast cell function-associated antigen (MAFA).
                                                                                                                                                                /note= "Asn is N-glycosylated"
150. .152
/note= "Asn is N-glycosylated"
                                                                                                                                          97...99
/note= "Asn is N-glycosylated"
                                                                                                                                    note= "Asn is N-glycosylated"
                                                                                                        Location/Qualifiers
                                                                                                              7. .10 /note= "ITIM motif"
       AAW88265 standard; protein; 189 AA.
                                    (first entry)
                                                                                                                                                          .139
                                                                                                                            65. .67
                                                                                                                            Modified-site
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                                                                                         Homo sapiens.
                                     29-MAR-1999
                                                                                                                                                                                              WO9854209-A2
                                                                                                                                                                                                             03-DEC-1998.
                      AAW88265;
                                                                                                            Peptide
AAW88265
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29-MAY-1998;

98WO-GB001572.

(PEPT-) PEPTIDE THERAPEUTICS LTD.

97GB-00011148.

31-MAY-1997;

Williams DH; Lamont A, Lamers MBAC, Hewitt EL,

WPI; 1999-059806/05. N-PSDB; AAV84198. New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.

Disclosure, Fig 1; 44pp; English.

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This is the amino acid sequence of human mast cell function- associated antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198) encoding human MAFA can be obtained from myelogenous leuksemic cell line KU812 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW88277) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2 Alternatively spliced forms (see AAW88256-67) of human MAFA have been identified. Polypeptides and sproteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                            CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS
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                                                                                                                                                                                                                                                                Length 189;
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                                                                                                                                                                                                                                                                  100.0%; Score 1023; DB 2; 100.0%; Pred. No. 1.8e-98;
                                                                                                                                                                                                                                                                                                    0; Mismatches
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Matches 189; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi N, Mikayama
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N-PSDB; AAD18734.
                                                                                                                                                                                                                               Sequence 189 AA;
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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MARA) ligand on a target cell, and prevents or inhibits natural Killer (NK) - or T-cell-expressed cell surface MARA from binding to MARA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MARA binding to a ligand on a target cell. by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition an amount sufficient to inhibit cell surface MARA binding to the ligand on the target cell. The agent or the composition is useful for treating to tumour by stimulating the cytotoxic activity of an NK cell-or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell-or T-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is human MARA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarintic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CHZ constant region; immunoglobulin heavy chain; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antigon, eachi disorder; melanoma; carcinoma; sarcoma; rhemmatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
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                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1023; DB 4; 100.0%; Pred. No. 1.8e-98;
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2002US-00053530.
2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                                       189; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                           Sequence 189 AA;
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Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

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WPI; 2003-801317/75

New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

Disclosure; SEQ ID NO 196; 157pp; English.

The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin heavy chain CE comprising a binding domain polypeptide that is fused to the himse region polypeptide and an immunoglobulin heavy chain CE constant region polypeptide and an immunoglobulin heavy chain CE constant region polypeptide that is fused to the CE constant region polypeptide. The immunoglobulin himse region polypeptide comprises: a wild-type human 1ggl immunoglobulin himse region polypeptide derived from (a) having 30 m more cysteine residues; where the mutated human 1ggl immunoglobulin himse region polypeptide contains a cysteine residues, where the mutated human Iggl immunoglobulin himse region polypeptide contains of contains a cysteine residue, where the first cysteine is not mutated; a mutated human Iggl immunoglobulin himse region polypeptide contains of cysteine residue; and a mutated human Iggl immunoglobulin himse region polypeptide contains of cysteine residues; where the mutated human Iggl immunoglobulin himse region polypeptide contains of cysteine residues. The binding domain-immunoglobulin himse region polypeptide contains of cysteine residues. The binding domain-immunoglobulin himse region polypeptide contains of cysteine residues. The binding domain-immunoglobulin fusion protein; a capable of a Least one immunoglobulin fusion protein, a percombinant expression construct comprising the polymicleotide (specifically binding to a promogratic contains of construct, panding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the binding domain-immunoglobulin fusion protein; a recombinant expression construct. Producing the binding domain-immunoglobulin fusion protein or polymicleotide of operators or about of parting a malignant condition or a B-cell disorder, e.g. malanoma, accinome or sarcoma, theumatoid arching domain-immunoglobulin fusion protein and is also available in electronic format dired by the present entil

Sequence 189 AA;

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                                                                                                                                                                                                                LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
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     Length 189;
                                     Indels
Query Match 98.4%; Score 1007; DB 7; Sect Local Similarity 98.4%; Pred. No. 8.5e-97; Matches 186; Conservative 1; Mismatches 2;
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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated an agent which specifically binds to a mast cell function associated an agent which specifically binds to cell function associated killer (MK)- or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NR- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition on the subject, to NK or T-cell or the target cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating tumour by stimulating the cytocoxic activity of an NK cell or a cytotoxic tumour cell. The invention is also useful for inhibiting an activity of tumour cell. The present sequence is mouse MAFA protein
                                                                                                                                                                             Mouse, pharmaceutical composition, mast cell function associated antigen, MAPA, natural killer cell; NK; tumour; therapy, cytotoxic T-cell; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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                                                                                                                                           Mouse mast cell function associated antigen (MAFA) protein.
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55.6%; Pred. No. 6.7e-49;
iive 26; Mismatches 56
                                                                                                                                                                                                                                                                                                                          /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                      location/Qualifiers
                                 AAE11760 standard; protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 19; 49pp; English.
                                                                                                                                                                                                                 immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2000; 2000US-0190716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-2001; 2001WO-US008596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi N, Mikayama T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMI-) GEMINI SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611482/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD18735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 188 AA;
                                                                                                                                                                                                                                                                                                                                                            WO200170805-A2
                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001.
                                                                                                       18-DEC-2001
                                                                   AAE11760;
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                                                                                                                                                                                                                                                                                        Key
Domain
                                                                                                                                                                                                                                                    Mus sp.
                    AAE11760
RESULT
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N-PSDB; AAV84222.
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                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                   29-MAY-1998;
                                                                                                                                                                                              WO9854209-A2
                                                                                                                                                                                                                                                      31-MAY-1997;
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                                                                                                                                                                                                                                                                                         EL,
                                                                                                                       Rattus sp.
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                                                                                                                                                                                                                                                                                            Hewitt
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                                                                                                                                                          Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSL-RILTNSLIQRCGAIHRNGLQASSCEVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                   Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention
                                                                                                                                                                                                                                                                                                                                                                                                                          A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                         Mammalian mast cell function-associated antigen (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 525.5; DB 2
Pred. No. 1.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      of inflammatory and allergic reactions.
                                                                                 AAR77033 standard; protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 37; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.4%; Sco
53.5%; Pre
tive 29;
                                                                                                                                                                                                                                                                                                                       Tal M;
                                                                                                                                                                                                                                                                                           RES & DEV CO LTD
                                                                                                                                                                                                                                                       95WO-US004258
                                                                                                                                                                                                                                                                         94IL-00109257.
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100; Conservative
                                                                                                                                                                                                                                                                                                                       Guthmann MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|:||
QWICEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGVCKKV 187
                181 HGVCKKV 187
                                    QWICKKV 186
                                                                                                                                                                                                                                                                                                                                         WPI; 1995-366356/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT01471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 188 AA;
                                                                                                                                                                                                                                                                                           (YEDA ) YEDA R
(RYCU/) RYCUS
                                                                                                                                                                                               Rattus rattus.
                                                                                                                                                                                                                 WO9527734-A1
                                                                                                                                                                                                                                                       06-APR-1995;
                                                                                                                                                                                                                                                                         08-APR-1994;
                                                                                                                       01-FEB-1996
                                                                                                                                                                                                                                   19-0CT-1995.
                                                                                                                                                                             prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                       Pecht I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of rat mast cell function-associated antigen (MAFA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFA molecule (see AAW88256) and to the discovery of splice variants (see AAW88266-67) of human MAFA that are not found in rat. Polypeptides and synthetic peptides (see AAW882566-67) and polymucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                Mast cell function-associated antigen; MAFA; splice variant; rat; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
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                                                                                                                                                                         Rat mast cell function-associated antigen (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.4%; Score 525.5; DB 2
53.5%; Pred. No. 1.7e-46;
ive 29; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                82. .84
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis and asthma), and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lamont A,
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEPT-) PEPTIDE THERAPEUTICS LTD
AAW88277 standard; protein; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-00011148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-GB001572,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases, and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.55
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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187

181 HGVCKKV

180 QWICEKV 186

Dp.

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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MARA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MARA from binding to MARA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MARA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition or a subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MARA binding to the ligand on the target cell. The agent or the composition is useful for treating at tumour by stimulating the cytocoxic activity of an NK cell- or a cytocoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The present sequence is rat MARA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
                                                                                                                                                                                                                                                                                                                                                           Rat; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
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                                                                                                                                                                                                                                                                                            function associated antigen (MAFA) protein.
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                                                                             AAE11761 standard; protein; 188 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fakahashi N, Mikayama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD18736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200170805-A2
                                                                                                                                                                                                                                                                                            Rat mast cell
                                                                                                                                                                                                                      18-DEC-2001
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                                                                                                                                                AAE11761;
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RESULT 7

AAE11761

ID AAE1

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AAC AAE1

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DT 18-1

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DT 18-1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of human mast cell function- associated antigen (MAFA) splice variant huWAFA(B3/4-), which lacks the C-lectin-like domain of human MAFA (see AAW88265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail. Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTDSVIYSMLELPTATÇAQNDYGPQQKSSSSRPSCSCLVAIALGLLTAVLLSVLLYQWIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90; Gaps
                                                                                                                                                                                                         Mast cell function-associated antigen; MAFA; huMAFA(E3/4-); splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             э.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 431; DB 2;
Pred. No. 5.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                             Human MAFA splice variant huMAFA(E3/4-).
                                                                                 AAW88267 standard; protein; 99 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                (PEPT-) PEPTIDE THERAPEUTICS LID
                                                                                                                                                                                                                                                                                                                                                                                                    97GB-00011148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.1%;
50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 50.3
nes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamers MBAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HGVCKKVRL 189
    180 QWICERY 186
                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-059806/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV84200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 99 AA;
                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 000
                                                                                                                                                                                                                                                                                                     WO9854209-A2
                                                                                                                                              29-MAR-1999
                                                                                                                                                                                                                                                                                                                                      03-DEC-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hewitt EL,
                                                                                                                 AAW88267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                 RESULT 8
                                                                   AAW88267
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Gaps

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human; inflammation; allergy; asthma; rheumatoid arthritis; tumour;
                                                                                                                                                         Lamont A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM14192 standard; protein; 35 AA.
                                                                                                                                                                                                                                                             Disclosure, Fig 2; 44pp; English.
                                                                                                                                    (PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded by probe
                                                                                            98WO-GB001572.
                                                                                                                 97GB-00011148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.0%;
Best Local Similarity 82.9%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COGSNYSTCASCPSCP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                        Hewitt EL, Lamers MBAC,
                                                                                                                                                                            WPI; 1999-059806/05.
                                                                                                                                                                                       N-PSDB; AAV84199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70 AA;
                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                    WO9854209-A2
                                                                                            29-MAY-1998;
                                                                                                                 31-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                         03-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM14192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
            therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                             Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergy; allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mast cell function-associated antigen; MAFA; huMAFA(E3-); splice variant;
                                                                                                                                                                                                                                                                                                                                                                          Novel DNA encoding a mast cell function-associated antigen (WAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                     A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
                                                                                                                          Partial sequence of mast cell function-associated antigen (MAFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 370.5; DB 2; Length 114;
Pred. No. 1.4e-30;
8; Mismatches 28; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MAFA splice variant huMAFA(E3-).
                                                             AAR77472 standard; protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 38; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW88266 standard; protein; 70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.2%; Scol
58.4%; Prec
tive 18; 1
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                                                                                                                                                                                                                                                                                           RES & DEV CO LID
                                                                                                                                                                                                                                                                      94IL-00109257.
                                                                                                                                                                                                                                                   95WO-US004258
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                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66; Conservative
                                                                                                                                                                                                                                                                                                                         Guthmann MD,
          99
                                                                                                                                                                                                                                                                                                                                             WPI; 1995-366356/47.
HWVCKKVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT01471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114 AA;
                                                                                                                                                                                                                                                                                                    RYCUS A.
                                                                                                                                                                                      Rattus rattus
                                                                                                                                                                                                                                                                                           (YEDA ) YEDA
                                                                                                                                                                                                          W09527734-A1
                                                                                                                                                                                                                                                                      08-APR-1994;
                                                                                                                                                                                                                                                 06-APR-1995;
                                                                                                      01-FEB-1996
                                                                                                                                                                                                                              19-0CT-1995
                                                                                                                                                                 prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW88266;
                                                                                 AAR77472;
          16
                                                                                                                                                                                                                                                                                                                         Pecht I,
                                                                                                                                                                                                                                                                                                   (RYCU/)
                                                   AAR77472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW88266
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This is the amino acid sequence of human mast cell function- associated antigen (MARA) splice variant humARA(B3-). humARA(B3-) is a major transcript, not found in rat, but highly expressed in human lung and granulocyte-enriched blood cells. The truncated protein includes the intracellular and transmembrane regions of human MARA (see AAW88265), collowed immediately by a polyproline motif (see AAW88264) due to a reading frameshift. This unique motif (see AAW88264) due to a reading frameshift. This unique motif has been used to design peptides (see AAW88259-64, AAW88268-72) that inhibit T cell antigen receptor-dependent activation induced by interleukin-2 (IL2) secretion from human cells. Inhibition of IL2 production prevents T cell proliferation and suppresses the immune system. These peptides, truncated MARA polypeptides including humARA(B3-), and polynucleotides encoding them, can be used be used in compositions for the treatment of inflammatory and allergic used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
                                                                                                                                                                                                                                             New polypeptide having a sequence corresponding to human mast cell intuction-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSRPSCSCLVAIALGLLTAVLLSVLLYQWIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 306.5; DB 2;
Pred. No. 3.5e-24;
1; Mismatches 5;
     DH;
Williams
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1;

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04-OCT-2000; 2000GB-00024263.
                                                                               Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488897/53.
                                                                                                                      WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM26602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
AAM26602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human single exon nucleic acid probes (SENP: see AA110068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 35
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Pred. No. 3.1e-15;
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100.0%; Pred. No. J...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 19018; 487pp; English
                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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30-JUN-2000; 2000US-0208408
03-MUG-2000; 2000US-020832366;
21-SEP-2000; 2000US-0234689P.
27-SRP-2000; 2000US-0234689P.
                                                                               2001WO-US000670
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Les 35; Conservative
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WO200157278-A2
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                                       09-AUG-2001
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                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome-derived single exon nucleic acid probes useful for analyzing
expression in human placenta.
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                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 25774; 639pp + Sequence Listing; English.
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100.0%; Pred. No. 3.1e-15;
iive 0; Mismatches 0;
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                                                           Rank DR;
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(MOLE-) MOLECULAR DYNAMICS INC
                                                        Chen W,
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2000US-0207456P.
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21-SEP-2000; 2000US-0234687P.
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2000GB-00024263.
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les 35; Conservative
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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                   Gaps
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                                                                                                                                                                Length 35;
                                                                                                                                                                                               Indels
                                                                                                                                                            Score 217; DB 4; I
Pred. No. 3.1e-15;
0; Mismatches 0;
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100.0%; Pre
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2000US-00608408.
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2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                                                               Conservative
                                                                                        human genetic disorders
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les 35; Conser
                                                                                                                           Sequence 35 AA;
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease.
encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                  for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human hearts.
                                                                                                                                            Gaps
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                                                                                                             Length 35;
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                                                                                                           Score 217; DB 4; 1
Pred. No. 3.1e-15;
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                                                                                                             21.2%; S
100.0%;
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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                                                                                                                            Similarity
                                                                               Sequence 35 AA;
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Best Local &
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Length 35;

DB 4;

Score 217;

0; Gaps 0; Best Local Similarity 100.0%; Pred. No. 3.1e-15; Matches 35; Conservative 0; Mismatches 0; Indels

64 SNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNS 98

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Search completed: August 10, 2004, 16:33:40 Job time : 54 secs

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                  Copyright
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OM protein - protein search, using sw model

Run on:

August 10, 2004, 16:35:05; Search time 53 Seconds (without alignments) 1118.605 Million cell updates/sec

US-09-811-367B-1 Title: Perfect :

1023 1 MTDSVIYSMLELPTATQAQN.....GLQASSCEVPLHGVCKKVRL 189 score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1291235 seqs, 313682936 residues Searched:

727970

Total number of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 189 Maximum I Maximum I

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

/cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep;* /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep;* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep;*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	.3678-1	96	3678-3 Semience 2 Appl				5/5 310 Sequence 310, App.					1-893-32 Seguence 32, April			2	70777	.807-6 Sequence 6. Appli
	ID	US-09-811-367B-1	US-10-207-655-196	US-09-811-367B-3	US-09-811-	US-09-864-	US-09-764-870-310	TIS-10-12E	173-00-010	TE-10 32E 000 10	CSC-01-SD	02-03-284	US-10-114	US-10-088	US-10-179	TIS-10-424	11000	US-09-944-807-6
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	Query Match Length DB	189	189	188	188	35	182	182	179	000	7 -	143	149	149	149	9		149
o40	Query Match	100.0	98.4	53.6	51.4	21.2	21.2	21.2	19.2	10.01	1.0	7.7	17.1	17.1	17.1	16.5	7 7 1	T.O.T
	Score	1023	1001	548.5	525.5	217	216.5	216.5	196.5	196.5	17.	1 .	175	175	175	168.5	160	5
	Result No.	н	2	ю	4	D.	9	7	80	o.	-	1 -	77	12	13	14	L T)

Semience 6	, ה	Semience 3, Appri	0	, 4	•	Segmence 340. App	Segmence 486. App	` `	Segmence 487. Ann	Segmence 466. Ann	Semience 466 Ann	0 00	Segmence 98. April	Semience 2 Appli	Semience 22 April	Segmence 76. April		Semience 10 April	Semience 83. Ann	Sequence 83. Appl	Seguence 67, Appl		Seguence 5855. An		80		1275		Sequence 471, App
.5 US-10-335-009-6	2 US-10-239-656-3	2 US-10-239-656-2	2 US-10-239-656-90	US-09-764-870-340	US-09-764-870-486	4 US-10-125-540-340	4 US-10-125-540-486	US-09-764-870-487	4 US-10-125-540-487	US-09-764-870-466	4 US-10-125-540-466	0 US-09-759-130B-98	6 US-10-741-790-98	4 US-10-270-470-2	3 US-10-114-893-22	2 US-10-262-839-76	4 US-10-212-198-9	4 US-10-212-198-10	0 US-09-759-130B-83			2 US-10-072-012-836			10 US-09-759-130B-108		2 US-10-296-115-1275	US-09-764-870-47	4 US-10-125-540-471
149 1	133 1	143 1	162 1	140 9	140 9	140 1	140 I	189 9	189 1	94	94 1	165 1	165 1	162 1	181 1	165 1	187 1	187 1	188 1	Н	r-1	Н	~	Т	145 1	• •	1 9	3	143 1
168 16.4	166 16.2	166 16.2	166 16.2	165 16.1	H	165 16.1			165 16.1		163.5 16.0				161 15.7	ın	··	6	159 15.5	· ·					157.5 15.4	•	57]	155.5 15.2	.5
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ALIGNMENTS

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APPLICANT: GENINI SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: ARahashi, No. US20020155110Aluaki
APPLICANT: ARahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshiduni
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THER TELLE REPRENCE: 021286/0278719
CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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; Pred. No. 3.5e-97;
0; Mismatches 0;
                    ; Sequence 1, Application US/09811367B ; Patent No. US20020155110A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.4
Matches 189, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                      GENERAL INFORMATION:
US-09-811-367B-1
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61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120

61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLBFCLARDSHLLVITDNQEMS

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Sequence 6, Appli

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Sequence 3. Application US/09811367B
Patent No. US20020155110A1
GENERAL INFORMATION:
APPLICANT: GEMINI SCIENCE, INC.
APPLICANT: TAKAHASHI, NO. US20020155110A1uaki
APPLICANT: Mikayama, Toshifumi
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAEA)
TITLE OF INVENTION: PRARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE FILE REPERENCE: 021286/0278719
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US-09-864-761-33902
US-09-864-761-33902
Sequence 33902, Application US/09864761
Fatent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Abarron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENER EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
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                                                                                                        61 CCGSKDSTCSHCPSCPILMTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
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  1 MIDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                                                                                                                                     121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.4%; Score 525.5; DB 9; 53.5%; Pred. No. 6.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rattus norvegicus
US-09-811-367B-5
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Best Local Similarity 53.5°
Matches 100; Conservative
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US-09-811-367B-5
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APPLICANT: GENINI SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
FILE REFERENCE: 021286/0278719
CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                        APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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55.6%; Pred. No. 2.9e-48;
iive 26; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1007; DB 14;
Pred. No. 1.6e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                 Sequence 196, Application US/10207655 Publication No. US20030118592A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09811367B
Patent No. US20020155110A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.4%;
Matches 186; Conservative
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Best Local Similarity 55.6
Matches 104; Conservative
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                                                                           181 HGVCKKVRL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                               RESULT 2
US-10-207-655-196
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US-09-811-367B-3
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5;

Gaps

19;

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64 SNYSTCASCPS-----CPDRWMKYGNHCYXFSVEEKDWNSSLEFCLARDSHLLVITDNQE 118
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| Publication No. US20030059875A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT214C1
| CURRENT APPLICATION NUMBER: US/10/125,540
| CURRENT PILING DATE: 2002-04-19
| Prior Application removed - See File Wrapper or Palm
| NUMBER OF SEQ ID NOS: 646
| SOFTWARE: PatentIN Ver. 2.0
| LENGTH: 182
                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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21.2%; Score 216.5; DB 9;
Best Local Similarity 35.0%; Pred. No. 4.6e-14;
Matches 48; Conservative 22; Mismatches 48;
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35.0%; Pred. No. 4.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : : | : : |
165 SKIFSETCSSVFKWICQ 181
                                                  Patent No. US20020042386A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-310
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ORGANISM: Homo sapiens
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Matches 48; Conserv
                                                                                          GENERAL INFORMATION:
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US-10-125-540-310
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 182
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OTHER INFORMATION: MAP TO ACO07436.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 18

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 13

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 30

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 6.1

OTHER INFORMATION: EXTHUMAN HIT: AAL88327.1, EVALUE 4.00e-15
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Pred. No. 5.3e-15;
CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-05

PRIOR PILING DATE: 2000-06-05

PRIOR APPLICATION NUMBER: US 60/23,366

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PLILING DATE: 2000-10-04

PRIOR PLILING DATE: 2000-10-04

PRIOR PELICATION NUMBER: US 60/236,359

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

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PRIOR PRILING DATE: 20
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21.2%; Score 21/; ub
Best Local Similarity 100.0%; Pred. No. 5.3
Matches 35; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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US-09-864-761-33902
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                                                              64 SNYSTCASCPS-----CPDRMMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQE 118
                                                                                       119 MSLLQVFLSEA-FCWIGLRNNS---GWRWEDGSPLNFSRISSNSFVQ-----TCGAINK 168
                                    Gaps
                                  19;
DB 14; Length 182;
                                 48; Indels
                                                                                                                                                                                                                                                                                                                  Sequence 130, Application US/09919039
Publication No. US20030108871A1
                                                                                                                                                                                                   169 NGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                        SKIFSETCSSVFKWICQ 181
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Gaps

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Indels

SNYSTCASCPSCPDRWMKXGNHCYYFSVEEKDWNS 35 64 SNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNS 98

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; Sequence 310, Application US/09764870

RESULT 6 US-09-764-870-310

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75 CPDRWMKYGNHCYYPSVEEKDWNSSLEFÇLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
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APPLICANT: MCCOY, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
APPLICANT: Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.2%
Matches 37; Conservative
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Best Local Similarity 32.2%
Matches 37; Conservative
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US-10-114-893-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 11
LENGTH: 149
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                 APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPERENCE: PA-0035 US 09/919,039

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR FPLICATION NUMBER: 60/222,113

PRIOR FPLICATION NUMBER: 60/222,113

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 EKDWINSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 QKTWNESRHLCASQKSSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEHTAWLWENGSAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
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Sequence 10, Application US/10335009
Publication No. US20040001804A1
Sequence 10, Application No. US20040001804A1
GENERAL INFORMATION:
APPLICANT: Portunelloor, Mathew A.
APPLICANT: BOLES, Kent S.
TILLE OF INVENTION. LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
FILE REFERENCE: 11707.02/469687-7
CURRENT APPLICATION NUMBER: US/10/335,009
CURRENT PILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 09/475,365
PRIOR FILING DATE: 1999-12-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 196.5; DB 10; Length; Pred. No. 5.2e-12; 25; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130
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SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.2%;
Best Local Similarity 32.7%;
Matches 53; Conservative 29
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US-10-335-009-10
                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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Best Local Similarity
Matches 53; Conserva
SENERAL INFORMATION:
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LENGTH: 179
                                                                                                                                                                                                                                  SEQ ID NO 130
LENGTH: 179
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APPLICANT: Treacy, Maurice
APPLICANT: Dewman, Michael R.
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikin
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
FILE OF INVENTION: SCRETEED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: G1 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 1090-10-06
ERRLIER PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CPDRWMKYGNHCYYFSVEBKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
                                                                                    APPLICANT: KALO, Seishi et al.
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAS TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AFILE REPRENENCE: GIN-6705CPUS CURRENT APPLICATION NUMBER: US/09/284,320 CURRENT PILING DATE: 1999-06-21 PRIOR APPLICATION NUMBER: UP 8-301429 PRIOR RILING DATE: 1996-11-13 PRIOR FILING DATE: 1997-11-07/P07/04056 PRIOR FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 CPYDWIGFQNKCYYFSKEEGDWNSSKYNCSIQHADLTIIDNIEEMNFIRRYKCSSDHWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.1%; Score 175; DB 10; Length 149; 32.2%; Pred. No. 6.8e-10; Live 24; Mismatches 48; Indels
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32.2%; Pred. No. 6.8e-10;
iive 24; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/10114893
Publication No. US20020193567A1
; Sequence 11, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
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US-10-424-599-222182
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APPLICANT: ITO., Koichi, ALGOLIA
APPLICANT: ISHIZUKA, Yoshiko
APPLICANT: ISHIZUKA, Yoshiko
FIILE REFERENCE: 2002-0400A/LC/00653
CURRENT APPLICATION NUMBER: US/10/088,859
CURRENT PILING DATE: 2002-05-29
PRIOR PELICATION NUMBER: PCT/JP01/06371
PRIOR FILING DATE: 2001-07-24
PRIOR PELICATION NUMBER: PCT/JP01/06371
PRIOR APPLICATION NUMBER: DP2000-222743
PRIOR APPLICATION NUMBER: JP2000-22743
PRIOR APPLICATION NUMBER: JP2000-254407
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
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94
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                                                                                  135 L---RNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shah, Purvi
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Mismatches
                                                                                                                                                                                         Sequence 2, Application US/10088859
Publication No. US20030148468A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10179528
Publication No. US20030166136A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                   FUJIMURA, Naoko
KOBAYASHI, Midori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Conservative
                                                                                                                                                                                                                                                APPLICANT: KATO, Seishi
APPLICANT: NAGATA, Naoki
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Best Local Similarity
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                                                                                                                                                                     US-10-088-859-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 149
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US-10-179-528-1
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APPLICANT: La ROSA Thomas J
APPLICANT: La ROSA Thomas J
APPLICANT: La ROSA Thomas J
APPLICANT: About K
APPLICANT: The Vibra
APPLICANT: The Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
ENGINERAL FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 95
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س
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llarity 32.2%; Pred, No. 6.8e-10;
Conservative 24; Mismatches 48;
                                                                                                                                ATTORNEY AGENT INCOMENTALY
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy 1
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0281 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFRAX: 415-85-0555
TELEFRAX: 415-85-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 39.3%; Pred. No. 1.8e-09;
Matches 33; Conservative 16; Mismatches 26
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NAME/KEY: unsure
LOCATION: (1)..(95)
OTHER INFORMATION: unsure at all Xaa locations
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Mismatches
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Publication No. US20040031072A1
GENERAL INFORMATION:
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 149 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: PITUNOT03
CLONE: 1756224
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ORGANISM: Glycine max
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es 37; Conserv
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RESULT 15
US-09-944-807-6
US-09-944-807-6

Sequence 6, Application US/09944807

Patent No. US20020119494A1

Patent No. US200201119494A1

Patent No. US200201119494A1

Patent No. US200201119494A07

TITLE DOF INVENTION: influence inflammatory conditions of chronic influence inflammatory conditions of chronic influence inflammatory accordations of chronic influence inflammatory accordations of chronic influence inflammatory accordations of chronic influence inflammatory conditions of chronic influence inflammatory conditions of chronic influence inflammatory accordance inflammatory conditions of chronic influence inflammatory accordance inflammatory accordance inflammatory accordance inflammatory influence inflammatory accordance inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammatory inflammato
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Search completed: August 10, 2004, 16:40:34 Job time : 55 secs

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Sequence 9, Appli
Sequence 9, Appli
Sequence 3, Appli
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Sequence 17, Appl
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Sequence 19, Appl
Sequence 19, Appl
Sequence 10, Appl
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Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 21, Appl
                                                              August 10, 2004, 16:32:44; Search time 18 Seconds (without alignments) 542.073 Million cell updates/sec
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Sequence 5, A
Sequence 23,
                                                                                                                          1023
1 MTDSVIYSMLELPTATQAQN......GLQASSCEVPLHGVCKKVRL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-722-126A-5
PCT-US95-04258-5
US-09-31-056A-23
US-08-722-126A-6
US-08-722-126A-6
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US-08-68-342-3
US-09-113-788-3
US-09-113-788-3
US-09-113-789-9
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US-08-772-126A-9
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US-08-772-126A-9
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            protein search, using sw model
                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                               Issued Patents AA:*
                                                                                                                 US-09-811-367B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
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1179
11799
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         Copyright
                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 189
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Match
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                                                                                                                           score:
                                                                                                                                                             Scoring table:
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430

430

3370.5

196.5

196.5

196.5

196.5

175.5

173.3
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169.5
169.5
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162.5
162.1
161.5
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                                            protein
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                                                                                                               Title:
Perfect :
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                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
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Sequence 8, App Sequence 10, App Sequence 15, App Sequence 15, App Sequence 14, App Sequence 20, App Sequence 21, App Sequence 2, App Sequence 2, App Sequence 25, App Sequence 25, App Sequence 2, App	CELL (FA)	Length 188;
155 15.2 115 3 US-08-722-126A-8 154 15.1 126 3 US-08-722-126A-8 152 14.9 78 4 US-09-731-056A-15 150 14.7 141 4 US-09-531-056A-16 150 14.7 187 4 US-09-535-521-17 148 14.5 14.4 174 2 US-09-535-521-17 147.5 14.4 174 2 US-09-535-521-17 147.5 14.4 174 2 US-09-531-056A-2 147.5 14.4 174 2 US-09-535-521-17 146.5 14.3 123 4 US-09-535-521-2 146.5 14.3 123 4 US-09-535-521-2 146 14.3 117 1 US-08-9481-676-2 147.5 14.3 117 1 US-08-481-676-2 148 14.3 117 1 US-08-481-676-2 149 13.9 77 4 US-09-531-056A-21	ALIGNMENTS 1. 22-126A-5 nnce 5, Application US/08722126A RRAL INFORMATION: PPLICANT: BCEHT, Israel PPLICANT: GUTHWANN, Marcelo D. PPLICANT: GUTHWANN, Marcelo D. PPLICANT: TAL, Michael TILE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MPRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: A19 Seventh Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CITY: Washington Street N.W., Ste. 300 CONFUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BALDABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: BRADABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: BRADABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: BRADABLE: Ploppy disk COMPUTER: BRADABLE: Ploppy disk COMPUTER: BRADABLE: Ploppy disk COMPUTER: BRADABLE: Ploppy disk CLASSIFICATION NUMBER: 11 109257 FILING DATE: 08-APR-1995 FILING DATE: 08-APR-1994 TORNEY/AGENT INFORMATION: RREFERENCE/DOCKET NUMBER: 25,618 RREFINING DATE: 08-APR-1994 TORNEY/AGENT INFORMATION: RREFERENCE/DOCKET NUMBER: 25,618 RREFINING PATE: 188 amino acids TYPE: Annion acids TYPE: Annion acids TYPE: Protein	Match 51.4%; Score 525.5; DB 3; ocal Similarity 53.5%; Pred. No. 1.1e-48;
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72 US-08-72	Query Best I

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GENERAL INCOMMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DRA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: DB20 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 PSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVIIDNQEMSLLQVFLSEAFCW 60
121 LLQVFLSBAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08722126A
Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington Strate: D.C. COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
                                                                                                                                                                                                                              Sequence 23, Application US/09531056A Patent No. 6455683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 IGLRNNSGWRWEDGSP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                   181 HGVCKKV 187
                                                                                                                             180 QWIČEKV 186
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Best Local Similarity
Matches 75; Conserv
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US-08-722-126A-6
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                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                            61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                          61 CCGSKGFMCSQCSRCPNLMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLITFPDNQGVN 120
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                                                                                                                                                                                                                      121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
                                              1 MIDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                                                      1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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        1; Gaps
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53.5%; Pred. No. 1.1e-40;
tive 29; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
PCT-US95-04258-5
; Sequence 5, Application PC/TUS9504258
; GENERAL INFORMATION:
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA);
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA);
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
        57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
           29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRANTS: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 amino acids
amino acid
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Best Local Similarity 53.59
Matches 100; Conservative
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TELEKA: 202-737-3528
TELEX: 24863
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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QWICEKV 186
                                                                                                                                                                                                                                                                                                         181 HGVCKKV 187
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           100;
             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 370.5; DB 3; Length 114; 58.4%; Pred. No. 2.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PALENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: 11 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT-1 PCT
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL ITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                           18; Mismatches
                                 NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REPERENCE/DOCKET NUMBER: PECHT=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROWDY AND NEIMARK
                ATTORNEY/AGENT INFORMATION:
FILING DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
                                                                                                                                                                                            LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                           66; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 419 Sever
CITY: Washington
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                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                    ; MUNDECULE 11F
US-08-722-126A-6
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PCT-US95-04258-6
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                                                                                        75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
                                                                                                               1 CPNLWARNGSHCYYFSMEKEDWNSSLKFCADKGSHLITFPDNQGVNLFQEYVGEDFYWIG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
                                              1; Gaps
                                                                                                                                                                              135 LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
                                                                                                                                                                                                      61 LRDIDGWRWEDGPALSLS-ILSNSVVQKCGTIHRCGLHASSCEVALQWICEKV 112
  DB 5; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 179;
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                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
TITE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
Query Match 36.2%; Score 370.5; DB 5; Best Local Similarity 58.4%; Pred. No. 2.6e-32; Matches 66; Conservative 18; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.2%; Score 196.5; DB 1; 32.7%; Pred. No. 2.4e-13; iive 25; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FASKISO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   US-08-690-095-9
; Sequence 9, Application US/08690095
; Patent No. 5792648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 32.77,
Thes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 179 amino acids amino acids
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Conservative
                 TITLE OF INVENTION: NONUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
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                                                                                                             Palo Alto
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CLONE: 1098616
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                                                                          ADDRESSEE:
                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-688-342-3
                                                                                                             CITY: P
STATE:
                                                                                             STREET:
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 179;
                                            Sequence 2, Application US/08650578
Patent No. 5811284
GENERAL INFORMATION:
APPLICANT: Aramburu Beltran, Jose
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Index-Botet, Miguel
APPLICANT: Phillips Jr., Joseph H.
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.2%; Score 196.5; DB 2; Best Local Similarity 32.7%; Pred. No. 2.4e-13; Matches 53; Conservative 25; Mismatches 69;
                                                                                                                                                                                                                                       ...ukESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTX: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,339
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0391
TELECOMMINICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFRAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08688342
Patent No. 5871964
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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US-08-650-578-2
                                   US-08-650-578-2
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93 EKDWNSSLEFCLARDSHLLVITDNOEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.

APPLICANT: Goli, Surya K.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Mismatches
E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0095-1 CIP
                                                                                                                                                                                        COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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Sequence 17, Application US/08772440

Patent No. 6046158
GENERAL INFORMATION:
APPLICANT: Azizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRIFIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE 78
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                                                                                                                                                                                                                                                                                                                                                                                                                              19.2%; Score 196.5; DB 3; 32.7%; Pred. No. 2.4e-13; tive 25; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                   PF-0110 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/772,440 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    NAME: Billings, Lucy J.
REGITATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parker, David L. REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17:
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                  ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                               LENGTH: 179 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. Box 4433 CIIY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512/474-7577
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                                                                                                                                                                                                                                                            single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               LIBRARY: GenBank
CLONE: 1098617
                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Texas
  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                       US-09-113-789-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWGYRCNCYFISSE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPORWMKYGNHCYYFSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 --SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09113789
Patent No. 6034219
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
ITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: Palo Alto
                                                                                                                                                                                                                                                                                  PF-0095-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTEM: DOS.
SOFTWARE: FASTESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
PILING DATE:
                                          SOFTWARE: FASTERO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
                                                                                                                                                                                                                                   NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-05
TELECOMMUNICATION INPORMATION:
TELEPAN: 415-845-055
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-09-113-789-9
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Gaps

15;

Length 179; Indels

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RESULT 13
US-08-772-440-16
US-08-772-440-16
is Sequence 16, Application US/08772440
is Patent No. 6046158
is GENERAL INFORMATION:
APPLICANT: Takashima, Akira
itTLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1, AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF SEQUENCES: 42
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
      78 RWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCW-IGL- 135
                                48 HWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFLGLS 107
                                                                                          136 --RNNSGWRWEDGSPIN----FSRISSNSFVQTCGAI-----NKNGLQASSCEVPLHGV 183
                                                                                                                    78 RWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCW-IGL- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 HWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQINESLSYFLGLS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QERQSQGKGVC----WTLRLWSAAVISMLL-----LSTCFIASCVEKMWGCCPN 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 QOKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILLCQGSNYSTC--ASCPS----CPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/772,440 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 435 ATTORNEY AGENT INFORMATION: NAME: Parker, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parker, David L. REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTN TELECOMMUNICATION INFORMATION: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 -- RNNSGWRWEDGSPLN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | |: | : | : | 1.08 DPQGNGKWQWIDDTPFS 124
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Best Local Similarity 30.7*
Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, W
STREET: P.O. Box 443
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                     168 CEMKKIYL 175
                                                                                                                                                                             184 C--KKVRL 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THERROF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               71 SCPS------CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQE 118
                                                                                                                                                                                                                                                                                                                            25 QQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYSTC--ASCPS----CPD 77
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                                                                                                                                                                           Gaps
                                                                                                                                                                         27;
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                                                                                                                                 Length 168;
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                                                                                                                                                                      51; Indels
                                                                                                                                                                                                                25 QQKSSSSKPSCSCLVAITLGLLTAVLLS------VLLYQWILCQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FLING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTD:493
TELEPHONE: 1512/418-3000
                                                                                                                          17.2%; Score 175.5; DB 3; 28.4%; Pred. No. 4e-11; tive 28; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                119 MSLLQVFLSEAFCW-IGLRNNSGWRWED 145
                                                                                                                                                                                                                                                                                                                                                                                                               123 QNFITQQLNESLSYFLGLSNPSKWGWND 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-772-440-15; Sequence 15, Application US/08772440; Patent No. 6046158; GENERAL INFORMATION:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 512/4747577
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
                                                                                                                                                                      42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, Whi
STREET: P.O. Box 4433
CITY: Houston
                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-772-440-15
                                                               TOPOLOGY:
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US-08-772-440-17
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                                                                                                                             Query Match
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72 CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 WIGVERNSSHHPWYTMNGLAFKHEIKDSDNAELNCAVLQVNRLKSAQCGSSIIYHCK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.6%; Score 169.5; DB 3; Length 120; 31.6%; Pred. No. 1.1e-10;
                                                                                                               DNA and amino acid sequence specific for natural killer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOTTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/543,246B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY,AGENT INFORMATION:
NAME: KASSENOÉF, MELVYD M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEOPHONE: 908-522-6927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches
                                                                                                                                                         NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
                                                                                                                                                                                                                                                                                                                      CONTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DNA and amino TITLE OF INVENTION: natural killer
              Sequence 18, Application US/08543246B
Patent No. 6262244
GENERAL INFRMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                             TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-543-246B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-543-246B-17
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US-08-543-246B-18
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DNA and amino acid sequence specific for natural killer cells

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72 CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 WIGL-RNNSGWRWEDGSPLNFSR--ISSNSFVQTCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 WIGVERNSSHHPWVTWNGLAFKHEIKDSDNAELNCAVLQVNRLKSAQCGSSIIYHCK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 CGHCPEEWITYSNSCYYIGKERRTWEESLLACTSKNSSLLSIDNEEEMKFLSIISPSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.6%; Score 169.5; DB 3; Length 135; 31.6%; Pred. No. 1.3e-10; tive 20; Mismatches 55; Indels 5.
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118-7704/PCT/CONT
       CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                           PRICATION DATA:
PRICATION AND DATA:
APPLICATION NUMBER: US 07/676,663
PILING DATE: 28-MAR-1991
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRICATION NUMBER: US 08/122,514
PRICATION NUMBER: US 08/122,514
ATTORNEY/AGENT INFORMATION:
NAMME: KASSENOFÉ, MELVYN M.
REGISTRATION NUMBER: 26,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: August 10, 2004, 16:35:49
Job time : 18 secs
                                                                                                                                                                                ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 118-
TELECOMMUNICATION INFORMATION:
TELEFRONE: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 135 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: C-terminal
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-543-246B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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(010/8) AMDI8 @BDA SIMI

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

August 10, 2004, 16:39:40; Search time 13.5 Seconds (without alignments) 1339.556 Million cell updates/sec Run on:

US-09-811-367B-3

1029 1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

95185 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1 2 6 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	mast cell function	agkisacutacin beta	C type lectin, B l	coagulation factor	beta	hepatic lectin hom	natural killer cel	aggretin alpha cha		coagulation factor	agkisacutacin alph	botrocetin beta ch	perlucin - Halioti	hepatic lectin hom	bitiscetin beta ch	coagulation factor	pancreatitis-assoc	lectin BRA3-2 prec	in bet	lectin BRA3-1 prec	pancreatitis-assoc	+-	lectin, galactose-	pancreatitis-assoc		щ	coagulation factor	pancreatic stone p	alpha
		ID	159421	JC7135	T28141	JC4691	JC7105	WMVZF2	T28140	PC7027	A47267	B42972	JC7134	B47267	S78774	WMVZF8	JC5059	JC4690	\$29822	LNRC3	JC2415	LNRC1	A49616	A28351	A38609	S54979	A41719	A34313	O.	4575	JC5058
		图	0	N	N	~	N	Н	2	2	7	7	7	7	7	Н	N	7	7	Н	7	Н	7	7	7	7	N	Н	7	7	N
	,	Match Length	188	146	156	146	146	167	170	144	133	123	152	125	155	116	125	152	175	162	123	162	175	165	135	174	175	163	129	166	131
ø	Query	Match	81.4	15.9	15.1	14.8	14.2	13.4	13.3	13.1	11,6	11.4	11.1	11.0	10.6	10.4	10.3	10.1	10.0	10.0	6.6	6.6		9.5	9.4	9.2	9.1	9.0	8.8	8.8	8.7
		Score	838	163.5	155.5	152.5	146.5	138	136.5	135	119	117.5	114.5	113.5	109.5	107.5	105.5	104	103	102.5	101.5	101.5	101	97.5	97	95	94	93	91	90.5	90
	Result	No.	П	2	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29

regenerating islet	regenerating islet	regenerating prote	pancreatic thread	tokaracetin beta c	hepatic lectin hom	reg I, regeneratin	ovocleidin - chick	alboaggregin-B alp	lectin CEL-I, N-ac	pancreatitis-assoc	lectin - barnacle	hypothetical prote	echinoidin - sea u	hypothetical prote	reg II, regenerati
RGHU1A .	RGHU1B	I83377	A37194	856007	WMVZEL	A47148	878596	B56829	JC7786	A48689	S10548	T30745	A26697	T28809	B47148
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166 1	166 1	174	175	40	143	165	142	40	140	174	173 2	159	147	166	173
														7.3 166	
		8.4		8.3	7.9	7.9		7.7	7.7	7.6	7.5	7.4	7.3		7.3

ALIGNMENTS

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SULT	9421

RESULT 1 159421 mast cell function associated antigen - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-011-1996 #sequence_revision 02-011-1996 #text_change 05-Nov-1999
C;Date: 02-011-1996 #sequence_revision 02-011-1996 #text_change 05-Nov-1999
C;Accession: 159421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is A;Title: A secretion inhibitory signal transduction molecule on mast cells is A;Teference number: 159421; MUID:96016176; PMID:7568140
A;Accession: 159421
A;Accession: 159421
A;Accession: 159421
A;Accession: 159421
A;Genetics: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
A;Genetics: A;Genetics: mafa

another C

ö Gaps ; 0 Length 188; 21; Indels tch 81.4%; Score 838; DB 2; al Similarity 80.7%; Pred. No. 1.3e-74; 151; Conservative 15; Mismatches 21; Query Match Best Local Similarity Best Loca Matches

셤

61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120 δ

임

121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180 g à

181 WICKKVL 187 ö

WICEKVL 187 181 g

RESULT 2

agkisacutacin beta chain precursor - sharp-nosed viper
NyAlternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Decies: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence-revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7135; PC7038
E;Cheng, X;; Qian, Y;; Liu, Q;; Li, B.X.Y; Zhang, M; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venomaly. A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Molecule type: mRNA

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A, Accession: UC4691
A, Molecule type: mRNA
A, Residues: 1-146 < MATIA
A, Forestion: UC4691
A, Molecule type: mRNA
A, Cross-references: DBBJ:DB332; NID:g1402641; FIDN:BAA11888.1; FID:g1402642
A, Cross-references: venom
R, Atoda, H.; Hyuga, M.; Morita, T.
B, Biol. Chem. 266, 14903-14911, 1991
A, Title: The primary structure of coagulation factor IX/factor X-binding protein isolate otein, tetranectin, and lymphocyte for epsilon receptor for immunoglobulin E.
A, Reference number: A39332; MUD:91332000; PMID:1831197
                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: B39332
A;Aolecule type: protein
A;Residues: 24-146 <ATO>
R;Atoda, H.; Ishikawa M.; Yoshihara, E.; Sekiya, F.; Morita, T.
B;Ochem. 118, 965-937, 1995
A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flama, A;Reference number: JC4329; MJID:96318509; PMID:8749314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: JC7705
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet a
A;Reference number: PC7027; MUID:99443731; PMID:10512747
                               two-chain anticoagulant protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWNSSLKFCADK--GSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 NWADAENFCTQQHAGGHLVSFQSSEEADFVVKLAFQTFGHSIFWMGLSNVWNQCNWQWSN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 DWNSSLKFC--ADKGSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI----DGWRWEG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggretin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: (3-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGRFIFMSFGFLVVFL-----SLSGTAADCPSD---WSSYEGHCYKPFSEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SLSGTGADCPSG---WSSYEGHCYKPFNEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: JC4330
A,Molecule type: protein
A,Molecule type: protein
A,Residues: 24-146 <AT2.
C,Superfamily: tetranectin, C-type lectin homology
C,Keywords: anticoagulant; blood coagulation; lectin; venom
E;1-23/Domain: signal sequence #status predicted <SIG.
F;24-146/Product: factor IX/X binding protein chain B #status P;25-142/Domain: C-type lectin homology <LCH.
F;25-142/Lomain: C-type lectin homology scales
F;25-142/Lomain: C-type lectin homology scales
F;25-142/Lomain: C-type lectin homology scales
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Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-ch
A;Reference number: JC4690; MUID:96184662; PMID:8645314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Residues: 1-146 <CHU>
A, Experimental source: venom gland
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: disulfide bond; platelet aggregation; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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larity 24.5%; Pred. No. 1.2e-07;
Conservative 25; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.2%; Score 146.5; DB 2 29.0%; Pred. No. 4.7e-07;
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39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ciype lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T2841
R;Milne, S.; Kaufman, J.; Beck, S.
Bobmitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility compl
                                                                                                                                                                                                                                                                                                                                                                                                 ė
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 TWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKWSD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-156 <MIL>
A;Residues: 1-156 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG----WRWEGGPALS- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 WTSSONNCSALGASLAVPDSAEDLSFTMRHKGSSPHWVGLSR-EGKEHPWEWVNRSPLSH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CPSCPILWTRNGSHCYYFSMEKKD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coagulation factor IX/factor X-binding protein chain A precursor - habu C;Species: Trimeresurus flavoviridis (habu) C;Species: Trimeresurus flavoviridis (habu) C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000 C;Accession: JC4691, B39332; JC4330 R;Atsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------SLSGTAADCPS---EWSSYEGHCYKPFDEPK
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                              A;Molecule type: protein
A;Residues: 24-50,59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTCSFVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPALSLRILINSLIQRCGAIHRNGLQASSCEVALOWICK 184
                                                                                                                                                                                                                                                                                                                               15.9%; Score 163.5; DB 2; 30.2%; Pred. No. 1e-08; ive 15; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LRILINSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 LFQVQGDGL---CAYLGDAGLSSSHCSTRRNWVCTK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 AMVALGLLTVILMSLLMYQRILCCGSKDSTCSH--
                                                        Experimental source: venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AVFTVLLITAVAFAVQAFQ-
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                         Cross-references: GB:AF176421
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.24
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 16
A; Introns: 17/1; 74/3; 110/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 39; Conserv
                                                                              PC7038
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                                                                                        A; Accession:
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predicted <MAT>

44

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Gypecies: Calloselasma rhodostoma (Malayan pit viper (fragment)
Cypecies: Calloselasma rhodostoma (Malayan pit viper)
Cypecies: Calloselasma rhodostoma (Malayan pit viper)
Cypecies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
CyAccession: PC7027
RyChung, C.H.; Au, L.C.; Huang, T.P.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet a A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: PC7027
A;Accession: PC7027
A;Accession: PC7027
A;Accession: CHUNA
A;Residues: 1-144 < CHUNA
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A; Residues: 1-133 <UGA>
A; Residues: 1-133 <UGA>
A; Estidues: 1-134 <UGA>
A; Estidues: 1-134 <UGA
A; Note: sequence extracted from NCBI backbone (NCBIP:124085)
B; Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Su;
Biochemistry 30, 1957-1964, 1991
A; Fitle: Isolation and chemical characterization of two structurally and functionally d:
A; Reference number: A37958; MUID:91129280; PMID:1993206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorrocetin alpha chain - jararaca
N;Alternate names: two chain botrocetin alpha chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: A47267; B37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pa;Reference number: A47267; MUID:93157385; PMID:8430107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 WLISOKDELADEDYVWIGLRAQNXEQQCSSEWSDGSSVSYENLIDLHTXKCGALEKLTGF 123
107 WIGLEVSTNQWKWVDNSSYNSTESDNLSVMEN----RCGTFKONTKVEGDVCSGEHQWVCQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 DSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFC--ADKGSHLLTFPDNQGVKLFG 123
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A; Residues: 1-40 <FUJ>
C; Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C; Complex: heterodimer of alpha electin homology
C; Reywords: hemagglutinin; heterodimer; venom
F; 2-128, Domain: C-type lectin homology LCH>
F; 2-138, Domain: C-type lectin homology ALCH>
F; 2-13, 30-128, 103-120, Disulfide bonds: #status experimental
F; 80, Disulfide bonds: interchain (to beta-75) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; Score 135; DB 2;
ilarity 25.5%; Pred. No. 6.3e-06;
Conservative 23; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | :: | : | | 124 RKWUNYYCEQMHAFVCKLLPY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 QA---SSCEVALQWICKKVLY 188
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es 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A47267
                                                                                                                      185 K 185
                                                                                                                                                                                                    163 K 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
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instural killer cell receptor homolog - chicken (fragment)

c;Species Gallus gallus (chicken)

c;Species: Gallus gallus (chicken)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T28140

C;Accession: T28140

S;Mille, S.; Kaufman, J.; Beck, S.

submitted to the EMBL Data Library, May 1998

A;Description: DNA sequencing and analysis of the chicken major histocompatibility compl

A;Reference number: Z20475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fowlpox
                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: fowlpox virus
C;Species: 30-6ep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: B29963
R;Tomley, F; Binns, M; Campbell, J; Boursnell, M.
Gen. Virol. 69, 1022-1040, 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of A;Reference number: JT0442; MUID:88229622; PMID:2836548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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A;Experimental source: clone cB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQCVKLFGEYLGQDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLLCPQFWRLLGDRCYELSTEKGNWTQAKMKCENLQSQLAVLRKKAEEDHLQQMAGAEFV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 WIGLR-NIDGWRWEGGPAL----SLRILTNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 DWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL---RNIDGWRW-----EGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 NWADAERFCKLOPKHSHIVSFQSAEEADFVVKLTRPRLKANLVWMGLSNIWHGCNWQWSD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatic lectin homolog (BamHI-ORF2) - fowlpox virus (isolate HP-438[Munich])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: B29963
A,Nolecule type: DNA
A,Residues: 1-167 <TOM>
A,Residues: 1-167 <TOM>
A;Residues: 1-167 <TOM>
A;Cross-references: GB:D00295, NID:g221380, PIDN:BAA00192.1, PID:g221383
C;Superfamily: fowlpox virus hepatic lectin homology, C-type lectin homology
C;Reywords: early protein
F;49-152/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62; Indels
                                                                                                                              146 GPALSLRILTNSLIQRCGA---IHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                        105 GARLINYKDWQEQ--SECLAFRGVHTEWLN-MDCSSTCSFVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not resolved (incomplete sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.4%; Score 138; DB 1; 27.1%; Pred. No. 3.7e-06; iive 28; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T28140
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-170 cMIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 PALSLRILINSLIQRCGAIH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | :::|: | 128 NDICLLFDTSNIIEMSCIFH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 27.1 tes 38; Conservative
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A;Map position: 16
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Best Local S:
Matches 38
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F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>
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Matches
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                                                                                                                                                                                                                                                                                                                                                                          C;Species: Vipera russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C;Accession: B42972
R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S. J. Biol. Chem. 267, 14109-14117, 1992
A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A nd A;Reference number: A42972; MUID:92332516; PMID:1629211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agkisacutacin alpha chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: UC7134; PC7037
R;Cheng, X; Qian, Y; Liu, Q; Li, B.X.Y; Zhang, M; Liu, J.
B;Cheng, X; Qian, Y; Liu, Q; Li, B.X.Y; Zhang, M; Liu, J.
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom A;Accession: UC7134; MUID:20025379; PMID:10558903
                                                                                                                                                                                                                                                                                                                                                     coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper
                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PATWIGLGNM--WKDCRMEWSDRGNVKYKALAEESYCLIMITHEKEWKSMICNFIAPVVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 DFYWIGLRNIDGWR-----WEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWIC 183
                                                                                                            | | | : | : | : | : | : | CPSGWSSYEGNCYKFFQQRANWADAERFCSEQAKGGHLVS-----IKIYSKEKDFVGDL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VKLFGEYLGQ
                                                                           CPILWTRNGSHCYYFSMEKKDWNSSLKFCAD--KGSHLLTFPDNQGVKLFG---EYLG--
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                                 Gaps
                                                                                                                                                                          128 -----QDFY-WIGLR--NID----GWRWEGGPALSLRILTNSLIQRCGAIHRN 168
                                                                                                                                                                                                                 VTKNIQSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKD 109
                                 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 123;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCAD--KGSHLLTFPDNQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Note: sequence extracted from NCBI backbone (NCBIP:108408) C;Superfamily: tetranectin; C-type lectin homology C;Keywords: hydrolase; wetalloproteinase; venom; zinc F;4-121,Domain: C-type lectin homology <LCH>F;4-121,Domain: C-type lectin homology <LCH>F;4-15,32-121,98-113/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: venom gland
A;Accession: PC7037
A;Molecule type: protein
A;Resiques: 24-53;84-86;A7-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C·type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
                            33;
     0.00021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 117.5; DB 2
Pred. No. 0.00027;
5; Mismatches 61
                               Mismatches
     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%; Scor
26.4%; Pred
tive 15; I
                               26;
25.4%;
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                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Moldcule type: protein
A;Residues: 1-123 <TAK>
A;Experimental source: venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Contents: V. r. siamensis
A; Accession: B42972
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Matches 32; Conserv
     Best Local Similarity
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Decreoesin Deta chain - jararaca (jararaca)

Discreoesin Deta chain - jararaca (jararaca)

C;Species: Bothrops jararaca (jararaca)

C;Species: Bothrops jararaca (jararaca)

C;Species: Bothrops jararaca (jararaca)

C;Species: Bothrops jararaca (jararaca)

C;Species: Bothrops jararaca (jararaca)

C;Species: Bothrops jararaca (jararaca)

C;Accession: B47267; C37958

R;Usami, Y.; Fulimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.

Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993

A;Reference number: A47267; MUID:93157385; PMID:8430107

A;Reference number: Drotein

A;Residues: 1-125 cUSA>

A;Residues: 1-125 cUSA>

A;Residues: 1-125 cUSA>

A;Residues: Lose extracted from NCBI backbone (NCBIP:124086)

A;Residues: Lose extracted from NCBI backbone (NCBIP:124086)

R;Fuljmura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Su Biochemistry 30, 1957-1964, 1991

A;Title: Isolation and chemical characterization of two structurally and functionally discense number: A37958; MUID:91129280; PMID:1993206

A;Residues: 1-40 cFUJA

C;Complex: heterodimer of alpha (see PIR:A47267) and beta chains

C;Superfamily: tetranectin; C-type lectin homology

C;Seywords: hemaggglutnin; heterodimer; venom

F;2-121/Domain: C-type lectin homology c;CMP>

F;2-13,30-121,98-113/Disulfide bonds: #status experimental

F;75/Disulfide bonds: interchain (to alpha-80) #status experimental
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                                                                                                                                                                                                                                                                                                                 45 TWADAESPCTKQVNGGHLVSIESSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQCSI 104
                                                                                                                                                                                               --SLSGTAADCSSG---WSSYEGHCYKVFKQSK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CPPDWSSYEGHCYRFFKEWMHWDDAEFFCTEQQTGAHLVSFQSKEEADFVRSLTSEMLKG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  perlucin - Haliotis laevigata
C;Species: Haliotis laevigata
C;Species: Haliotis laevigata
C;Sacession: S78774
S;Mann, K.
R;Mann, K.
submitted to the Protein Sequence Database, January 2000
A;Reference number: S78774
A;Cottents: S78774
A;Accession: S78774
                                                                                                                                    35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADK -- GSHLLTFPDNQGV -- -- KLFGEYLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                    ---YWIGLR----
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      Length 152;
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                                                                                                                                                                                                                                                                 95 DWNSSLKFCADK--GSHLLTFPDNQGVKLFGEYLGQDF---
   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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1 Similarity 31.3%; Pred. No. 0.00069;
26; Conservative 12; Mismatches 32
11.1%; Score 114.5; DB; 23.6%; Pred. No. 0.00067
                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | :: | :: | E---WSDGSSISYENWIEEESKKCLGVH 129
                                                                                                                                                                                                                                                                                                                                                                                                     DGWRWEGGPALSLRILINSLIQRCGAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 DFYWIGLRNIDGW----RWEGG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B47267
botrocetin beta chain - jararaca
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                           Local Similarity
nes 35; Conserv
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   Query Match
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